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AC012107 Homo sapi
AL139089 Human DNA
AL196266 Human DNA
AC010801 Homo sapi
AC012239 Homo sapi
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www-shgc.stanford.edu

Quality: Phrap Quality: y=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.3.

NOTE: Transposon sequencing failed to verify the number of repeat copies 67315-69359. Unsure number of repeat copies 67315-69359. Unsure number of repeat copies 67315-69359.

NOTE: Shatter libraries failed to resolve dinucleotide repeat region 171590-171722. Unsure number of repeat copies

171590-171722. Forced join 171695.

Location/Qualifiers
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Submitted (07-0CT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 187064)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (16-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 16, 2002 this sequence version replaced gi:15022008.
Draft Sequence Produced by DOE Joint Genome Institute
Draft Sequence Produced by DOE Joint Genome Conter
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DOE Joint Genome Institute

Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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   CTAAAAATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGG
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                    AGCAGAGTGAGACKCCGTCTCAAAAACAACAACAAAAAAACAAAAAAAACCATAAGACATTG
                                                                                  AGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTG
                                                                                                                                  CTAAAAATACAAAAATAGCTGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGG
                                                                                                                                                                                                GATCACCTGAGGTCAAGAGTCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTA
                                                                                                                                                                                                                                                               CCAGGCATGACACTGGCTGAATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCG
                                                                  AGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTG
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="NOTE: Transposon sequencing failed to verify the number of repeat copies 67315-69359. Unsure number of repeat copies 67315-69359."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="CTC-550B14"
67315...69359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="NOTE: Shatter libraries failed to resolve dinucleotide repeat region 171590-171722. Unsure number of repeat copies 171590-171722. Forced join 171695."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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Pred. No. 5.2e-128;
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Sequencing vector: M13; 84*
Sequencing vector: plasmid; 16*
Chemistry: Dye-primer ET; 84* of reads
Chemistry: Dye-terminator Big Dye; 16* of reads
Chemistry: Dye-terminator Big Dye; 16* of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199676 bases at least Q40
Consensus quality: 200928 bases at least Q30
Consensus quality: 201749 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 236000; agarose-fp
Insert size: 204523; sum-of-contigs
Quality coverage: 6.54 in Q20 bases; agarose-fp
Quality coverage: 7.57 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC019238 204340 bp DNA linear HTG 17-AUG-2000 Homo Bapiens chromosome 19 clone RP11-700B5, WORKING DRAFT SEQUENCE, 12 unordered pieces.
AC019238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH0700B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University School of Medicine, MO 63108, USA
On Aug 17, 2000 this sequence v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 204340) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone Unpublished
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                             s: gap of unknown length
s: contilg of 7953 bp in length
s: gap of unknown length
s: contilg of 9281 bp in length
s: gap of unknown length
s: gap of unknown length
s: contil of 10459 bp in length
                        gap of
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Best Local Similarity
Matches 231; Conserv
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                                             Conservative
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clone_end:SP6
vector_side:left"
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/estimated_length=unknown
52281. .65275
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41059. .52180
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155779. .155878
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/mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                        22639. 155778
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22539. .122638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_name:Contig23"
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1853. .5901
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65375: gap of unknown length
95161: contig of 29786 bp in length
95261: gap of unknown length
122538: contig of 27277 bp in length
122638: gap of unknown length
152638: gap of unknown length
155778: contig of 33140 bp in length
155878: gap of unknown length
155878: gap of unknown length
204340: contig of 48462 bp in length.
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99.1%;
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                                           1;
                                                               Score 231; DB 12;
Pred. No. 8.9e-69;
                                             Mismatches
                                             1;
                                                                                   Length 204340;
                                             Indels
                                           0;
                                        Gaps
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JOURNAL REFERENCE REFERENCE AUTHORS TITLE

AUTHORS TITLE

Direct Submission

JOURNAL

COMMENT

41059

30500 30400

6002 12966 13066 21019 21119

2753 2853 5902

ACCESSION VERSION

CEYWORDS

ORGANISM

iominidae; Homo

RESULT 2 AC019238

DEFINITION

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Length 184822;

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Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.

* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence on tigs
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Produced by Berkeley Web Site: http://pga.lbl.gov Center Code: PGABERK Center Project Name: W033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-AUG-2003) Genome Sciences, Lawrence Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, U 3 (bases 1 to 184822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 184822)
Cheng, J.-F., Hamilton, M., Peng, Y., Peng, Z., Malinov, I. and Rubin, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC146499.1 GI:34013545
HTG; HTGS_PHASE2; HTGS_DRAFT.
Aotus nancymaae (Ma's night monkey)
                                                                                                                                                                                                                                                                                                                                                                                                This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-NOV-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheng, J.-F., Hamilton, M., Peng, Y., Peng, Z., Malinov, I. and Rubin, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cebidae; Aotinae; Aotus.
1 (bases 1 to 184822)
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AC146499
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                                                                                                                             Sequencing vector: Plasmid; pUC18
                                                                                                                                                        Summary Statistics:
                                                                                                                                                                                                Funding agent: Programs for Genomic Applications (NHLBI)
                                                                                                                                                                                                                                                                                                             The order-orientation of the draft sequence was accomplished
                                                                                                                                                                                                                                                                                                                                                         http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheng, J.-F., Hamilton, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAAAACAACAACAACAAAAAAACAAAAAAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCAC 65495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCAC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone Name:
                                                                                                                                                                                                                                                                   (http://baboon.math.berkeley.edu/mavid),
                                                                                                                                                                                                                                            (http://lagan.stanford.edu/) and paired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184822 bp
clone CH258-450E24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH258-450E24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Peng,Y.,
Rubin,E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mukherjee,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA linear
WORKING DRAFT
                                                                                                                                                                                                                                              end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hosseini, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berkeley National
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SEQUENCE, 2
                                                                                                                                                                                                                                              information
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SOURCE
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VERSION
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DEFINITION
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AC146898
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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Pongo pyg
                                                                                                                          Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, B.H., Masiello, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Pearson, R., Portnoy, M.B., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Croen, P.
                                                                                                                                                                                                                                                                                                                                                           Hominidae; Pongo.

1 (bases 1 to 232406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC146898.3 GI:38638702
HTG; HTGS_PHASE2; HTGS_DRAFT.
    Direct Submission
                         Green, E.D
                                                                Unpublished
                                                                                        NISC Comparative Sequencing Initiative
                                                                                                            Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pongo pygmaeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pongo pygmaeus (orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC146898
                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the gaps between them are based on estimates provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available the accession number will be preserved.

1 32135: contig of 32135 bp in length 32136 32235: gap of unknown length 32236 184822: contig of 152587 bp in length 10cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATCAC--GAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGAACCCAGGAGGCGGAGGTTGCACTCCAGCCTGGGTAACAAGAGTGAAACTCTGTCT 133549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGCATGGTGGCATGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGTCAGGAGAATTG 133609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGAGACCATCCTGGTCAACATGGTGAAAACCCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAAACAACAACAAAAAAACAAAAAAACCATAAGACAT
                                         (bases 1 to 232406)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pygmaeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Aotus nancymaae"
/mol_type="genomic DNA"
/db_xref="taxon:37293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .184822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone
                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232406 bp
CH253-50L14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 161.2; DB 1
Pred. No. 4.7e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358
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DRAFT SEQUENCE, 4 ordered
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Masiello,C.,
, Pearson,R.,

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FEATURES
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                        misc_feature
                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in 020 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a bran-daring and the sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-OCT-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 232406)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the accession number will be preserved.

1 80408: contig of 80408 bp in length
80409 80508: gap of unknown length
101957: contig of 21449 bp in length
102057: gap of unknown length
102058 206149: contig of 104092 bp in length
206150 232406: contig of 26157 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 231482 bases at least 040
Consensus quality: 231897 bases at least 030
Consensus quality: 232064 bases at least 020
Insert size: 245000; agarose-fp
Insert size: 232106; sum-of-contigs
Quality coverage: 21.15x in Q20 bases; sum-of-contig;
Quality coverage: 22.32x in Q20 bases; sum-of-contig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a Phrap-derived quality score.
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Contact: nisc_zoo@nhgri.nih.gov
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/estimated_length=unknown
80509..101957
/note="assembly_fragment"
101958..102057
                                                                                                                                             vector_side:left"
                                                                                                                                                                                     clone_end:T7
                                                                                                                                                                                                                                                                                                               /mol_type="genomic DN
/db_xref="taxon:9600"
/clone="CH253-50L14"
                                                                                                                                                                                                               note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                              organism="Pongo pygmaeus"
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                 'clone_lib="CH253"
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                                                                                         Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geralgery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Maldrim, J., Molla, M., Morriow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Ye, W. J., Zhao, J., and Zody, M.
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Submitted (19-AUG-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 97676)
                                                                              Direct Submission
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-952N18
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	n Male BAC"	Ewan, P., McGurk, A., Macqunald, P., Marquis, N., leus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., or, J., Norman, C.H., O'Connor, T., O'Donnell, P., ara, Y., Norman, C.H., O'Connor, T., O'Donnell, P., ara, Y., Raymond, C., Riley, R., Rogov, P., Rothman, D., R., Schauer, S., Severy, P., Spencer, B., N., Stojanovic, N., Subramanian, A., Trigilio, J., volore, J., Tirrell, A., Travers, M., Trigilio, J., volore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., volore, J., Tirrell, A., Travers, M., Trigilio, J., volore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., X., Wyman, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., X., Wyman, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., X., Wyman, D., Ye, W.J., volore, J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, M., Zimmer, A. and Zody, M., Zimmer, J., Zimmer, A. and Zody, M., Zimmer, D., Ye, W.J., volore, J., Zimmer, A. and Zody, M., Zimmer, J., Zi	baum, C., Lander, E., Abraham, H., Allen, N., Bastien, V., Beda, F., Barna, N., Bastien, V., Beda, F., Er, B., Brown, A., Burkett, G., Choepel, Y., Colangelo, M., Collins, S., eArellano, K., Dewar, K., Diaz, J.S., e. M., Ferreira, P., FitzHugh, W., Gage, D., inde, S., Goyette, M., Graham, L., Hagos, B., Heaford, A., Horton, L., Chason, R., Jones, C., Kann, L., Karatas, A., mazares, R., Landers, T., Lehoczky, J.,
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 5, 2001 this sequence version replaced gi:12581050.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                   AL445686 107868 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RPII-496D1 on chromosome 1 Contains the gene for a novel protein (FLJ45258), a ribosomal protein L26 (RPL26) pseudogene, the 5' end of the SRRWI gene for serine/arginine repetitive matrix 1 and a CpG island, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAAACAACAACAAAAAAAAAAAAA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTGAACCCAGGAGGGGAGGTTGCACTCCAGCCTGGTTAACAAGAGTGAAACTCCATCT 36372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGCATGGTGGCACATGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAAGACCAGCCTGGCCAACATGGAGAAACTCCGTCTCTACTAAAAATAGAAAAATTAGC
                                                                                                                                                                                                             (bases 1 to 107868)
                                                                                                                                                                                                                                                                                                                             FLJ42528; RPL26; SRRM1.
                                                                                                                                                                                                                                                                                                             sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="MER20"
20009. .20057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (21315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="AluSp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="MLT1E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family="MLT1E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ement (23597. .23885)
family="AluSc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="L2"
                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "MLT1E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 160; DB 5;
Pred. No. 9.3e-44;
l; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 97676;
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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-496D1 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Wellcome Trust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="RP11-496D1.2-001"
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Sw:Q9UNX3 Tr:BAC21653 Tr:BAC56365"
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TVVLILLKMYNRKMRTRRELEPKGPKPTAPSAVGPNSNGSQHPATVTFSPVDVQVETR
                                                                                                                                                                                                                                                                                                                                            locus Loy- ... protein" product="novel protein" /note="match: cDNAs: Em:BC050474.1" /note="match: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61043. .62761)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62295. .62764)
/locus_tag="RP11-496D1.1-002"
join(42900. .43060,48860. .48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="RP11-496D1.1-001"
/note="Clone_left_end: RP11-373M8"
join(42900. .43060,48860. .48953,54376.
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                                                                                         db_xref="GI:55959942"
/db_xref="UniProtKB/TrEMBL:Q5T1S8"
                                                                                                                                                                                       product="novel protein"
protein_id="CAI14681.1"
                                                                                                                                                                                                                                                                                                                             locus_tag="RP11-496D1.
standard_name="OTTHUMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="ribosomal protein L26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="RP11-496D1.1-001"
product="novel protein"
note="match: cDNAs: Em:AK124
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/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              locus_tag="RP11-496D1.1-001"
oin(9547. .9605,48860. .48948,54376.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Clone_right_end: RP4-594I10"
oin(9547. _9605,48860. .48948,54376.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locus_tag="RP11-496D1.1-002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2295. .62764)
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                                                                                                                                                                                                                                                                                                                                  _name="OTTHUMP00000003372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Em: AK124519.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .48953,54376.
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62744. .62749 /locus_tag="RP11-496D1.1-002"

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2697,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="serine\/arginine repetitive matrix 1"
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/gene="match: 1007864.18:18954. .19163, AL445648.18:19750. .20835)
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join(9533) . 96783,99420 . 995209,100103 . .100225,
102295 . 102465,103407 . .103522,104845 . .105048,
105870 . .106064,106349 . .106468,AL445648.18:2423 . .2697,
AL4445648.18:8287 . .8367,AL445648.18:8878 . .8964,
AL445648.18:10228 . .10372,AL445648.18:14383 . .11493,
AL445648.18:16591 . .17155,AL445648.18:17688 . .17883,
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join(96711. .96783,99420. .99509,100103. .100225,
102295. .102465,103407. .103522,104935. .105048,
105870. .105950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="RP11-373M8.1-007"
join(96708. .96783,99420. .99509,100103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Join(86502. .86535,99420. .99509,100103.
102295. .102465,103407. .103468)
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join(86502. .86535,99420. .99
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/note="match: ESTs: Em:AII23635.1"
join(86502. .86535.99420. .99509,100103. .100225
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join(85152. .85213,86455. .86
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join(85152. .85213,86455. .86!
/gene="SRRM1"
                                                                                                                                                                                                              /locus_tag="RP11-373M8.1-008"
/product="serine\/arginine repetitive matrix 1"
/note="match: ESTS: Em:AU142070.1"
/onin(96711. .96783,99420. .99509,100103. .100225
102295. .102465,103407. .103522,104935. .105048
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105870. .105950)
/gene="SRRM1"
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102295. .102391,103470. .103522,104845. .105048
105870. .105978)
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/product="serine\/arginine repetitive matrix 1"
/note="match: EST8: Em:AL693732.1 Em:AL704047.1
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105870. .105978)
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                                 Unpublished 2 (bases 1
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Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 10
AC016542
AC016542.11 GI:19744959
HTG.
      2 (bases 1 to 171480)
Smith, D.R.
                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                   Sequence Data
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Mammalia; Eutheria;
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/product="serine\/arginine repetitive matrix 1"
/note="match: ESTs: Em:BG700853.1"
/note="match: ESTs: Em:BG700853.1"
/poin 96729. .96783,99420. .99509,100103. .102465
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join(96729. .96783,99420. .99509,
,03407.__103522)
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join(96735. .96783,99420. .99)
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                                                                                                                                                                                                        144 AGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAATACAAAAAAATAGCTGG 203
                    321
                                                                                                                                                                                                                                                                                                                    222;
                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Street, Waltham, MA 02453, USA
On Mar 27, 2002 this sequence version replaced gi:16930889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-MAR-2002) Genome Therapeutics Corporation, Street, Waltham, MA 02453, USA 6 (bases 1 to 171480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-NOV-2001) Genome Street, Waltham, MA 02453, USA (bases 1 to 171480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-MAR-2002) Genome Street, Waltham, MA 02453, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-DEC-1999) Genome Therapeutics Corporation, Street, Waltham, MA 02453, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (09-APR-2002) Genome Therapeutics Corporation, 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, D.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                  Similarity
CAAAAACAACAACAAAAAAAAAAAAAACCATAAGACATTGTCCATCTGCGGTTCCCAGAC 380
                                                                                                                                                                                                                                                                        CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                 GAACCCAGGAGGCGGATTGGTTCTGCATTCTAGCCTAGGTGACAGAGTGAGACTCCGTCT
                                                                                                                                                 GCATGGTGGCACACCCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                                  AGACCAGCCTGGGCAACATGGTGAAACCCCCGTCTCTACTAAAAATATAAAAATTAGCTGG
                                                                                                                                                                                                                                                 CATGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACCTGAGGTCAGGAGTTCG 116855
                                                                              GATCGCAGAGTGAGCCGAAATCACAGATCACAG---AGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                 GCATGGTGGCATGTGCCTGTAATCCCAGCTACCCGGGAGGCTGAGGCAGGAGAATAGCTT 116975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 171480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 171480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 990315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The true right end of clone RP11-522H2 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: hg069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is the entire insert of clone RP11-354E23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: GT
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-354E23"
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                                                                                                                                                                                                                                                                                                                                  40.0%;
71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Therapeutics Corporation
                                                                                                                                                                                                                                                                                                                 Score 159.8; DB 5
Pred. No. 1.4e-43;
1; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Therapeutics
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                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                Length 171480;
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                                                   117035
                                                                                                                                                                                  116915
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HS408N23
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                               gene
                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117036 CAAAAAAAAAAAAAAAAAAGAAAAGGACCAATAGGAGAACAAAGTTTAAAAAGAA 117095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               one subclone; and the assembly was confirmed by restriction digest except on the rare occasion of the clone being a YAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Nov 2, 1997 this sequence version replaced gi:2462400. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. B-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chr22
RP3-408N23 is from the library RPCI-3 constructed by the group
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete sequence. Z98048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS408N23 97916 bp DNA linear PRI 18-MP Human DNA sequence from clone RP3-408N23 on chromosome 22q13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hunt,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z98048.1 GI:2582746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTGAAGG 117104
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complement(2630. .4351)
/locus_tag="RP3-408N23.3-003"
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                                                                                                                                                                                               /pseudo
                                                                                                                                                                                                                                                                                                           clone="RP3-408N23"
                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                        map="q13"
                                                                                                                                                                                                                                                                                                                                                                  chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .97916
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                                                       _start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 18-MAY-2005
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/locus_tag="RP3-362J20.1-001"

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mRNA
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                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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AL035450.1:39435. .39615,AL035450.1:41464. .41584,
AL035450.1:43371. .46534,AL080242.11:105. .3488)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(complement(34109...34299), complement(13937...13997), complement(9428...9494), complement(7439...7590), complement(AL049764.4:22070...22186), complement(AL049764.4:20289...20434), complement(AL049764.4:20289...20434), complement(AL049764.4:20101...20196), complement(AL049764.4:16998...17080), complement(AL049764.4:16998...17080), complement(AL049764.4:16918...17080), complement(AL049764.4:16918...14042))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="InterPro:IPR001993"
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55540. .55606,59753. .59823,63208. .63283,65737. .65794,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYGSFPGGFPGGMPGNFPGGMPGMGGGMPGMAGMPGLNEILSDPEVLAAMQDPEVMVA
FQDVAQNPANMSKYQSNPKVMNLISKLSAKFGGQA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               name="OTTHUMP00000028873"
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115. .3617,AL035450.1:24689. .24751
ACCESSION
VERSION
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ORIGIN

Ś В Š 당 á 밁 Ş В

DEFINITION

Homo sapiens chromosome 11 clone RP11-804A23 map 11, WORKING DRAFT SEQUENCE, 10 unordered pieces.
AC090344
AC090344.3 GI:14626339

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RESULT 9
AC090344/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                              81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                            CAAAAAAAAAAAAAAAA 11547
                                                                                                                          САЛАЛАСАЛСАЛСАЛАЛАЛ 339
                                                                                                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                     TGGGCATGGTGGCACATGCCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCA 11468
                                                                                                                                                                                                                                                           TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                          TCGAGATCAGCCTGGCCAACGTGGCGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.9%;
75.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 159.4; DB 5;
Pred. No. 1.5e-43;
1; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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AUTHORS
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E 2 (bases 1 to 195616)

E 3 birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,

Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J.,

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos; B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,

Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,

Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,

Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McRernan, K.,

McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,

Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,

O'Connell, P., O'Neil, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,

Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,

Roy, A., Santos, R., Schauer, S., Schupback, R., Steman, S., Severy, P.,

Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,

Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,

Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is architrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 7, 2001 this sequence version replaced gi:13357354. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.

1 (bases 1 to 195616)

Birren,B., Linton,L., Nusbaum,C. and Lander,B.

Homo sapiens chromosome 11, clone RP11-804A23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 804 A 23

Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 191318 bases at least Q30

Consensus quality: 193221 bases at least Q30

Consensus quality: 194120 bases at least Q20

Insert size: 194716; sum-of-contigs

Quality coverage: 9.4 in Q20 bases; sum-of-contigs
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                       be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                 9270
9370
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                                                                                                            9269:
9369:
10358:
10458:
13550:
9: contig of 9269 bp in length
9: gap of 100 bp
8: contig of 989 bp in length
0: contig of 3092 bp in length
0: gap of 100 bp
2: contig of 12572 bp in length
2: gap of 100 bp
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                                                180665. .19561
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                                                                                    note="assembly_fragment"
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contig of 2563 bp i
contig of 2563 bp i
gap of 100 bp
contig of 34199 bp i
gap of 100 bp
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gap of 100 bp
contig of 14476 bp i
gap of 100 bp
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91667 ATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCACTTGAGGTCAGGAGT 91608

81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140

Similarity

39.7%;

Score 158.8; DB 1 Pred. No. 3.5e-43; Mismatches

68;

Indels

7; Gaps

DB 12; Length 195616;

Conservative

141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC 200

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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., FitzHugh, W., Gard, Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McEvrnan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribe, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuper, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, M., Traviss, N., Trayislo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91427
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                                                                                                                                                                                                                                                                                   Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 11, 2001 this sequence version replaced gi:13357355. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 197156)
Birren,B., Linton,L., Nusbaum,C. and Lander,E
Homo sapiens chromosome 11, clone RP11-804B24
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Homo sapiens chromosome 11 clone RP11-804B24 map 11, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L12623
Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                 Center clone name: 804_B_24
                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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124356
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Consensus quality: 193219 bases at least Q40
Consensus quality: 194831 bases at least Q30
Consensus quality: 195508 bases at least Q20
Insert size: 196256; sum-of-contigs
Quality coverage: 10.0 in Q20 bases; sum-of-contigs
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182158
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/clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
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11469: gap of 100 bp
114984: contig of 3515 bp in length
15084: gap of 100 bp
21800: contig of 6716 bp in length
21900: gap of 100 bp
61396: contig of 39496 bp in length
61496: gap of 100 bp
83042: contig of 21546 bp in length
83142: gap of 100 bp
97779: contig of 14637 bp in length
97879: gap of 100 bp
124455: gap of 100 bp
124455: gap of 100 bp
150156: contig of 25701 bp in length
150256: gap of 100 bp
182157: contig of 31901 bp in length
182257: gap of 100 bp
182157: contig of 31901 bp in length
18257: gap of 100 bp
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Best Local Similarity
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                                                                                                                                                                                                            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. a Homo sapiens genomic DNA published Only in Database (1999)

2 (bases 1 to 197856)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. a Direct Submission
                                                                                             On :
                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@ssc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel.81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                        Submitted (25-NOV-1999) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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vector_side:right"
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                                                                      , 2003 this sequence version 
Location/Qualifiers
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182158. .182257
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L50157. .150256
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_xref="taxon:9606"
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74.0%;
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Pred. No. 3.5
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Submitted (15-JAN-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Homo sapiens chromosome 8 clone
                                                                                                   Direct Submission
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* NOTE: This record contains 84 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.
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                           Query Match
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Matches 216; Conserv
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                                                                                                                                                                      NOVEL COMPOSITIONS AND METHODS FOR CANCER PATENT: JP 2005510225-A 16 21-APR-2005; SAGRES DISCOVERY OS Homo Sapien PN JP 2005510225-A/16 PD 21-APR-2005 PF 02-DEC-2002 JP 2003546739 PR 30-NOV-2001 US 09/997722 PI david w maurice CC CC Location/Qualifiers.
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81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
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1 (bases 1 to 96593)
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JP 2005510225-A/16.
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NOVEL COMPOSITIONS AND METHODS
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                            Conservative
                                                                                                /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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4: contig of 742 bp in length
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7: gap of 100 bp
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7: gap of 100 bp
8: contig of 734 bp in length
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                         Score 158.4; DB 2;
Pred. No. 3.4e-43;
1; Mismatches 57;
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AX695641
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Novel compositions and methods for cancer
Patent: WO 03008583-A 1268 30-UAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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GTGAGACTTCATCTCAAAAAAAAACAAAAACAAAAAACAAAAAACCAACCAGATG 18504
                                                                                    TGAGATCGCAG-----AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGA 306
                                                                                                                               TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
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                        CTTGAACCCAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCAGCTTGGGTGACAAGC
                                                                                                                                                                        TCAAGATCAGCCTGGCCAACATGGTGAAACCCCCGTCTACTAAAAAATACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Discovery (US)
                                                                                                                                                                                                                                                                                                                                                            /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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Pred. No. 3.4e-43;
1; Mismatches 57
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WO03008583.
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RESULT 15 AC010677/c LOCUS

DEFINITION

AC010677 112659 bp Homo sapiens chromosome 7 clone

CTD-2304L4, complete sequence.

linear PRI 03-JAN-2002

DNA

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3 (bases 1 to 112659)
Waterston, R.H.
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University School of Medicine,
MO 63108, USA
On Nov 30, 2000 this sequence v
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4 (bases 1 to 112659)
Waterston, R.
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University School of Medicine,
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Submitted (17-SEP-1999) Genome
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1 (bases 1 to 112659)
Waterston, R.H.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: H_MS2304L04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: submissions@watson.wustl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:http:/
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Waterston, R.H.
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AC010677.4 GI:11465112
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="7"
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Pred. No. 3.7e-43;
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Submitted (18-JUL-2001) DOE Jo
Drive, Walnut Creek, CA 94598,
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DOE Joint Genome Institute and Stanford Human Genome Center
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WI-6759 G05738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.2.
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DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                TCAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATCAGC
                                                                                     TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
 TGGGCATGGTGGCAGGGCCTGTAATCCCCAGCTACTCAGGAGGCGGAGGTTGCAGTGAGC
                     TGGGCATGGTGGCACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-370J7"
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Submitted (03-MAY-2002) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
4 (bases 1 to 170154)
DOB Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 29, 2003 this sequence version replaced gi:27819471.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (22-JAN-2003) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut 5 (bases 1 to 170154)
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DOE Joint Genome Institute.
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DOE Joint Genome Institute,
Alamos National Laboratory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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Homo sapiens chromosome 16 clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC040168
                                                                                    Similarity
ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCAGATCAC--GAGGTCAAGAGA 134378
                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAAAAAAAAAAAAAGACA 95559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Joint Genome Institute, Stanford Human Genome Center and mos National Laboratory.
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                                                                                                                                                        /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-46107"
                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                  39.5%;
75.8%;
                                                                Score 157.8; DB 5; Pred. No. 7.3e-43; 1; Mismatches 63;
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ACCESSION
VERSION
KEYWORDS
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AUTHORS
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DE 3 (bases 1 to 186747)

SBirren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Liamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Comor, T., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
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1 (bases 1 to 186747)

Birren, B., Linton, L., Nusbaum, C. and Lander, E
Homo sapiens chromosome 16, clone RP11-764C24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-DEC-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
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Center clone name: 764 C 24

Center clone name: 764 C 24

Sequencing vector: M13, M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 174578 bases at least Q30

Consensus quality: 179739 bases at least Q30

Consensus quality: 182173 bases at least Q20

Insert size: 188000; agarose-fp

Insert size: 185347; sum-of-contigs

Quality coverage: 4.6 in Q20 bases; agarose-fp

Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
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138462: contig of 14706 bp in length
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180503: contig of 26837 bp in length
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Query Match Best Local S Matches 207 al Similarity 207; Conser 81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAAGA 140 39.5%; nilarity 75.8%; Conservative Score 157.8; DB 12; Length 186747; Pred. No. 7.6e-43; 1; Mismatches 63; Indels 2; G 2; Gaps

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                                                                                                                                                                                                                                                                                                         Submitted (23-DEC-2002) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94596 (Dases 1 to 198575)
DOE Joint Genome Institute, Stanford Human Genome Center and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
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                                                                                                                                                                                Drive, Walnut Creek, CA 94598, USA
On Mar 22, 2003 this sequence version replaced gi:27363205
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                               Submitted (22-MAR-2003) DOE Joint Genome Institute,
                                                                                                                                                                                                                                                                    Alamos National Laboratory.
Direct Submission
                                  Quality: Phrap Quality >=40 100% of Sequence Estimated Total Number of Errors is 0. NOTE: BACTERIAL TRANSPOSON excised at 8530.
                                                                                                                       Finishing Completed at National Laboratory
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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REFERENCE AUTHORS VERSION KEYWORDS RESULT 20 AL732374 COMMENT SOURCE ACCESSION DEFINITION JOURNAL TITLE ORGANISM Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 2, 2002 this sequence version replaced gi:23393869. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at Human DNA sequence from clone RP13-444K19 on chromosome X Contains a mitochondrial ribosomal protein S18C (MRPS18C) pseudogene, the 3' end of the gene for a novel protein similar to PHD finger protein 2 PHF2 and a CpG island, complete sequence. Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
RP13-444K19 is from the library RPCI-13.2 conf Pieter de Jong. For further details see http://www.sanger.ac.uk/Projects/C_elegans/wormpep was generated from part of bacterial clone contigs chromosome X, constructed by the Sanger Centre Chro Homo sapiens Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Eukaryota; Metazoa; Mammalia; Eutheria; AL732374.14 GI:23476649 HTG; CpG island; MRPS18C; PHF2. Contact: vega@sanger.ac Web site: Center code: SC Center: Wellcome Trust Sanger Direct Submission Chapman, J. Hominidae; Homo. Homo sapiens (human) VECTOR: pBACe3.6 (bases 1 to 224187) //www.chori.org/bacpac/home.htm http://www.sanger.ac.uk Genome Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Institute constructed Chromosome p This sequence s of human romosome X Mappi λ the group Mapping

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FEATURES
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (298051.7:6109. .6298),
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complement (200042. .200228), complement (196787. .196949),
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complement (179266. .179568), complement (17243. .172828),
complement (173431. .173609), complement (172743. .172828),
complement (171481. .171614), complement (170579. .170892),
complement (125845. .126181), complement (123347. .124911))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (171481 . .171614), complement (170579 . .170892), complement (148509 . .148604), complement (129799 . .129908), complement (125845 . .126181), complement (122347 . .124911))/gene="PHF8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA314327.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _tag="RP13-444K19.1-001"
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FOLM ALGRANDARSTARAPCOVFLTGRRPSVGSQSNQAGGKRPKKGLATAKQRLG
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202260. .202401,203326. .203486,207924. .>207927))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="PHF8"
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
TITLE
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VERSION
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AC150910/c
                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                  COMMENT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 GAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAA 90
Wilson,R.K.

Direct Submission
Submitted (09-OCT-2004) Genetics, Genome Sequencing Center,
Submitted (09-OCT-2004) Genetics, MO 63108, USA
Forest Park Parkway, St. Louis, MO 63108, USA
On Oct 9, 2004 this sequence version replaced gi:51241995.
                                                                                                                                Submitted (14-AUG-2004) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 169908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC150910 169908 bp
Pan troglodytes chromosome 7 clone
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                        Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC150910.2 GI:54019620
                                                                                                                                                                                                                                                                                          Jnpublished
                                                                                                                                                                                                                                                                                                                 The sequence of Pan troglodytes clone
                                                                                                                                                                                                                                                                                                                                           Vilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGAAAGAAAGAAAAGAAAAAA 191136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACTACACTCCA------GCCTGAGCĂACĂGĂGTGĂCĂCTCCCTCTCĂĂĂĂĂAĂĂA 191109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAAAAACAAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGGCCAATATGGTGAAAACCCCTGTCTGTACTAAAAATACAAAAATTAGCAGGGCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCAGCACTTTGGGAGGCCAAGGCAGGCAGATCACCTGAGGTCAGGAGTTCAAGACCAG 190938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTCTAAAAAAGTATTTCAAGAAATAATGGCAGCCTGGCGCGCGGTGGCTCATGCCTGTAA 190878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAAAAAACAAAAAAACCATAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCACATGCCTGTAATCCCAGCTGCTCGGGAGGCGGACACTGCAGTGAGCCGAGATCGCT 191058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGT 210
                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 169908)
                                                                                                                                                                                                                                                                  bases 1 to 169908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                   Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGKRPKKGLATAKQRLGRILKIHRNGKLLL"

complement (join(128280 .129067,129799 .129908,

148509 .148604,170579 .170892,171481 .171614,

172743 .172828,173431 .173609,179401 .178504,

179266 .179568,181358 .181447,185535 .185626,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHEDEIPETVRTVQLIKDLARBIRLVEDIFQQNVGKTSNIFGLQRIFPAGSIPLTRPA
HSTSVSMSRLSLPSKNGSKKKGLKPKELFKKAERKGKESSALGPAGQLSYNLMDTYSH
QALKTGSFQKAKFNITGACLNDSDDDSPDLDLDGNESPLALLMSNGSTKRVKSLSKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDDDDPALKSRPKKKKNSDDAÞWSPKARVTPTLPKQDRPVREGTRVASIETGLAAAAA
KLAQQELQKAQKKKYIKKKPLLKEVEQPRPQDSNLSLTVPAPTVAATPQLVTSSSPLP
PPEPKQEALSGSLADHEYTARNAFGMAQANRSTTPMAPGVFLTQRRPSVGSQSNQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTKIAKKVDKARLMAEQVMEDEFDLDSDDELQIDERLGKEKATLIIRPKFPRKLFRAK PCSDPNRVREPGEVEFDIEEDYTTDEDMVEGVEGKLGNGSGAGGILDLLKASRQVGGF PCYAALTEAPASPSTQEAIQGMLCMANLQSSSSSPATSSLQAWWTGGQDRSSGSSSSSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTVSNSPASQRTPGKRPIKRPAYWRTESEEEEENASLDEQDSLGACFKDAEYIYPSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 157.8; DB 5;
Pred. No. 8.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA linea:
CH251-484K21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 224187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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WORKING DRAFT
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: plasmid; 100% Chemistry: Dye-primez ET; 0% of reads Chemistry: Dye-primez ET; 0% of respective to the consensus of the consensus quality: 164720 bases at least Q30 Consensus quality: 16527 bases at least Q20 Consensus quality: 16527 bases at least Q30 Consensus quali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: C_AB0484K21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7532
21677
21777
34794
34894
54354
54454
88285
88385
125438
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1482
7432
54454. .88284
/note="assembly_name:Contig41"
                                                                                                                                      54354. .54453
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21777. .34793
                                                                                                                                                                                                      34894. .54353
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34794. .34893
                                                                                       estimated
                                                                                                                                                              note="assembly_name:Contig40"
                                                                                                                                                                                                                                          estimated_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_name:Contig38"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="CH251-484K21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21676: contig of 14145 pp in renyc...
21776: gap of unknown length
34793: contig of 13017 bp in length
34893: gap of unknown length
54353: contig of 19460 bp in length
54453: gap of unknown length
84284: contig of 3831 bp in length
88384: gap of unknown length
125437: contig of 37053 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125537: gap of unknown 169908: contig of 44371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _type="genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
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                                                                                                                                                                                                                                          length=unknown
                                                                                                                                                                                                                                                                                                                                                                                        _length=unknown
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1 bp in
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FEATURES

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gap

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RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                       Hominidae, Homo.

E 1 (bases 1 to 174097)

Murny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Mibrooke,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,

Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Davila,M.L., Davis,C., Dann,A.L., Ding,Y., Dinh,H.H.,

Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,

Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,

Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

Uarvia K. Hart.M., Havlak,P., Hawes,A., He,X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC069513.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC069513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC Library)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACO69513
ACO69513
HOMO sapiens 3 BAC RP11-171N2 (Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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Pred. No. 8.6e-43;
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REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE AUTHORS

JOURNAL TITLE

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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovat, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
May, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
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Tamerisa, K., Tang, H., Tansey, J., Taylor, C.,
Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L.,
Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S.,
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Wu, Y. F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and
Gibbas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley,K.C.

Direct Submission

Submitted (02-JUN-2000) Human Genome Sequencing Center, Department Submitted (02-JUN-2000) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One parties Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (28-SEP-2002) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 174097)
                        Worley,K.C.
Direct Submission
Submitted (15-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 28, 2002 this sequence version replaced gi:23343662.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                   of Molecular and Human
Baylor Plaza, Houston,
5 (bases 1 to 174097)
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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Direct Submission
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gc-help@bcm.tmc.edu
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USA
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JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

COMMENT

JOURNAL

REFERENCE AUTHORS

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. clones are only he remainder of

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. of a local database that includes entries from local mapping efforts. 7:541-550) searches dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequences similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

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FRATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
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note="AC069513:G/AC112775:A/AC124944:A"
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/chromosome="3"
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y 75.8%;
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Pred. No. 1e-4
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Direct Submission
Submitted (07-OCT 1999) Production Sequencing Facility, DOE Joi
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
3 (bases 1 to 209844) 2 (bases 1 to 209844)
DOE Joint Genome Institute. Hominidae; Homo.

1 (bases 1 to 209844)

DOE Joint Genome Insti Homo sapiens (human) 209844 bp DNA Homo sapiens chromosome 19 clone CTB-33G10, AC011495 DOE Joint Genome Institute and Stanford Human Genome Center Direct Submission Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Unpublished AC011495.8 GI:21747443 Institute and Stanford Human Genome Center complete Euteleostomi; PRI 14-JUL-2002 DOE Joint

REFERENCE AUTHORS

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COMMENT

Louis,

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Query Match
Best Local Similarity
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SEQUENCE, 21 unordered pieces.
ACO74388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 14, 2002 this sequence version replaced gi:15281207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (26-NOV-2000) DOE Joint Genome Institute,
Submitted (26-NOV-2000) DOE Joint Genome Institute,
Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-AUG-2001) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: Phrap Quality >=40 99.9% of Sequence; Estimated Total Number of Errors is 0.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finishing Completed at Stanford Human www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 (bases 1 to 209844)
DOE Joint Genome Institute and Stanford Human Genome
2 (bases 1 to 173556)
Waterston, R.H.
                                                           1 (bases 1 to 173556) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www.jgi.doe.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                            The sequence of Homo sapiens Unpublished
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                Homo sapiens
                                                                                                                                                                                               AC074388.2 GI:9690406
                                                                                               Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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Pred. No. 1.1e-42;
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.99319 Consensus quality: 158826 bases at least Q40 Consensus quality: 158318 bases at least Q30 Consensus quality: 163318 bases at least Q20 Consensus quality: 165604 bases at least Q20 Insert size: 16500; agarose-fp Insert size: 171556; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (30-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Aug 4, 2000 this sequence version replaced gi:9587428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 4.60 in Q20 bases; agarose-fp Quality coverage: 4.61 in Q20 bases; sum-of-contigs
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number be preserved.
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45343. .45442
                                               vector_side:left"
76092. .76191
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60169. .68196
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20451. .25976
/note="assembly_name:Contig26"
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|5824. .15923
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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173556: contig of 19392 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1615
                                                                                                                                                                                                                                                                                                                                                             1735 CAGGAGTGGTGGCACACCTGTAATTCCAGCTACTCAGGAGGATGAGGCAGGAGAATCA 1794
                                                                                                                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
Human DNA sequence from clone RP5-1155K23 on chromosome 1p31.3-32.3 Contains a Down syndrome critical region gene 5 (DSCR5) pseudogene, a ribosomal protein S15a (RP515A) pseudogene, a novel gene (FLJ10884), a ribosomal protein L36 (RP15A) pseudogene, a novel gene end of a novel gene, complete sequence.
                                                                                                                                                                                                                                                                                    CTTGAACCCAGGAGGCGGAGGTTGCAATAAGCCGAGACTTGCGCCACTGCGAGACTCTGTC
                                                                                                                                                                                                              TCAAAAAAATAAAATAAAATAAAAATAAAAAAAAAGGCACT 1894
                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                               TCAAAAACAACAAAAAAAAAAAAAAACCATAAGACATT 359
                                                                                                                                                                                                                                                                                                                         TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG-CAGAGTGAGACKCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87827. .87926
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87927. .99071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 157.2; DB 1
Pred. No. 1.2e-42;
1; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 173556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL ORGANISM Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:16973818.
The following abbreviations are used to associate primary accession AL162739.24 GI:21211651 HTG; DSCR5; FLJ10884; RPL36; RPS15A. HOmo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Direct Submission White, S. Hominidae; Homo. (bases 1 to 84001)

DEFINITION

1854

319

260

200 1734

COMMENT

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numbers given in the feature table with their source darabases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORWPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group, Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chr1
RP5-1155K23 is from the library RPCI-5 constructed by the group Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECTOR: PCYPAC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match: proteins: Sw:P57054 Tr:AAP35702 Tr:Q9JHG1"
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                                                                                                                                locus_tag="RP5-1155K23.3-001"
                                                                                                                                                                                                                                                                                                                                           pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    locus_tag="RP5-1155K23.2-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rocus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _tag="RP5-1155K23.1-001"
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                                                                                                                                                                                                                                                                .43661)
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REFERENCE
AUTHORS
TITLE
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AÇ025599/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CESSION
                                                                                                                                                                                                                                                                                                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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1 (bases 1 to 158330)
Birren,B., Linton,L., Nusbaum,C. and Lander,B.
Homo sapiens chromosome 8, clone RP11-508K19
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 8, clone RP11-508K19, complete sequence.
AC025599
AC025599.8 GI:18464214
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC025599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAAAAAAAAAAGAATAATAC 57459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACAACAACAAAAAACAAAAAAAA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTG-----TGCCATTGCACGCTAGCCTGGGCAACAAGAGTGAAACTCTATCTCAA 57484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTACTAAAAATACAAAATTAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGTAATCCCAGCACTTTGGGAGGCCAAGCTGGGCAGATCACCTGAGGTCAGGAGTTTG
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Em:CB980254.1 Em:CB900362.1 Em:CB960937.1 Em:CB96054
Em:R20871.1 Em:CB900362.1 Em:CD514723.1 Em:N5554
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join(complement(AL139343.9:68437. .68745),
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Pred. No. 1e-42;
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1 Em:AV688590.1
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgelter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgelter, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulne, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Melmga, V., Murphy, T., Naylor, J., Mayuen, C., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sepocer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wilson, B., Wilson, B., Wilson, D., Viel, R., Vo, A., Wilson, B., Wilson, B., Wilson, D., Ve, W.J., Young, G., Direct Submission

M., Submitted (10-EPRL, 2002) Whitchesd Tretting Auth Center for Common, J., Submitted (10-EPRL, 2002) Whitchesd Tretting Auth Center for Common, M., Stojanovic, J., Simmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 1, 2002 this sequence version replaced gi:18072197. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L5714
Center clone name: 508_K_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR Web site: http://www-seq.wi.mit.edu
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
    clone="RP11-508K19"
                                                                                                chromosome="8"
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RESULT 27 AC068995/c AC068995 AC068995 AC068995 AC068995 AC068995 AC068995 AC068995 AC068995 ACCESSION AC068995	Qy 238 AGGAGCCGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGAT 297	Qy 118 GCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCT 177	Query Match 39.2%; Score 156.8; DB 5; Length 18830; Best Local Similarity 71.0%; Pred. No. 1.6e-42; Matches 206; Conservative 1; Mismatches 83; Indels 0; Gaps 0; Qy 58 AGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGG 117	peat_region complement(2788134258) /rpt_family="L1PA7" peat_region 3435134381 /rpt_family="L1PA7" /rpt_family="AT_rich" peat_region complement(3566636486)	/ TPE family="MLFIC" repeat_region 26691. 26898 / TPE family="LIME1" repeat_region 2689926986 repeat_region 2706027467 repeat_region 2706027467 repeat_region complement (2746827777) repeat_region / TPE family="LIME1" repeat_region 2777827839 / TPE family="LIME1"	region region region	repeat_region 1704517462 repeat_region /rpt_family="MSTB" repeat_region complement(1807918366) /rpt_family="MATS" repeat_region /rpt_family="AluSx" repeat_region 1923519484 repeat_region /rpt_family="LINC4a" repeat_region /rpt_family="MIR" repeat_region 2210722167 /rpt_family="(CA)n" repeat_region /rpt_family="MIR" repeat_region /rpt_family="MIR" repeat_region /rpt_family="MIR" repeat_region 238223758

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 29, 2000 this sequence version replaced gi:11024742.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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HTG: HTGS_PHASE1; HTGS_DRAFT
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Sequencing vector: M13; LOB821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 160818 bases at least Q40
Consensus quality: 177694 bases at least Q30
Consensus quality: 18433 bases at least Q20
Estimated insert size: 185987; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
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                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                     Center project name: HBGH
Center clone name: RP11-463G10
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Quality coverage: 3.4x in Q20 bases; sum-of-contigs estimation
data.html)
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.) NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

189927 192638 192738 192738 188028 189827 184813 184913 187928 182500 182400 139583 147338 108664 120336 108564 180505 175833 180405 168187 168087 147438 139483 49757 63726 20159 20259 .55147 .30877 Location/Qualifiers 108663 78834: 49656: contig gap of contig gap of contig gap of gap of gap of gap of gap of contig gap of contig gap of contig gap of gap of contig gap of gap of contig gap o gap of unknown contig of 1097 contig of 1136 gap of unknown gap of unknown length contig of 20158 bp in gap of unknown length contig of 12378 bp in gap of unknown length gap of contig gap of contig of 13969 bp in conti of unknown ig of 3015 of unknown ig of 2711 of unknown ig of 2313 of unknown ig of 1799 of unknown length ig of 14909 bp in unknown of 5882 unknown of 6958 unknown of 7609 unknown of 7755 of 4572 unknown length of 10441 bp in length unknown length of 11672 bp in unknown length of 13210 bp in unknown length of 16419 bp in of 20158 bp in length unknown length of 1895 of 7546 of 8506 unknown unknown length
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VERSION
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                                                           111372 bp
Homo sapiens chromosome 1 clone
unordered pieces.
AL357146
                              AL353145.4 GI:9796994
HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                        AL353145
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Homo
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Pred. No. 1.8e-42;
1; Mismatches 83
                                                                              RP4-633K13 map
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                                                                              linear HTG 10-JUL-2001 map p34.3-36.11, 9
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                       misc_feature
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49802
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12509
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CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9213061.
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Chemistry: Dye-terminator Big Dye; 74% of reads
Chemistry: Dye-terminator ET-amersham; 24% of reads Consensus
Chemistry: Dye-terminator ET-amersham; 24% of reads Consensus
quality: 105338 bases at least Q0
Consensus quality: 107404 bases at least Q0
Consensus quality: 108616 bases at least Q20
Insert size: 110572; sum-of-contigs
Insert size: 124958; 7.7% error; agarose-fp
Quality coverage: 3.70x in Q20 bases; sum-of-contigs Quality
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Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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4: gap of 100 bp
5: contig of 9274 bp in length
8: gap of 100 bp
7: contig of 19409 bp in length
7: gap of 100 bp
1: gap of 100 bp
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gap of 100 bp
contig of 5471 bp in length
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contig of 5289 bp in length
gap of 100 bp
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COMMENT

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AC022252
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Best Local Similarity
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Perreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meddrim, J., Meneus, L., Morrow, J., Naylor, J., Morman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,
Homo sapiens, clone RP11-28012
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC022252 150934 bp DNA Homo sapiens clone RP11-28012, WORKING
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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fragment_chain:3"
93170. .105801
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75194. .80482
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105902. .111372
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fragment_chain:3"
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fragment_chain:2"
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Pred. No. 1.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: L4795

Center clone name: 28 0 12

Center clone name: 28 0 12

Center clone name: 28 0 12

Sequencing vector: M13, M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 132159 bases at least Q40

Consensus quality: 141146 bases at least Q30

Consensus quality: 144793 bases at least Q20

Insert size: 157000; agarose-fp

Insert size: 157000; agarose-fp

Quality coverage: 3.1 in Q20 bases; sum-of-contigs

Quality coverage: 3.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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7: contig of 364 bp in
7: gap of 100 bp
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13: gap of 100 bp
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gap of 100 bp
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contig of 1382 bp in length
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clone_end:T7
vector_side:right"
4758. .4857
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-28012"
                                                                                                                      estimated_length=100
|2137. .13936
                                                                                                                                                                                                        'note="assembly_fragment"
|0458. .10557
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'note="assembly_fragment"
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109294: contrig of 11156 bp in length
109394: gap of 100 bp
123250: contrig of 13856 bp in length
123350: gap of 100 bp
13459: contrig of 11309 bp in length
134759: gap of 100 bp
150934: contrig of 16175 bp in length.
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contig of 10036 bp in length
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g of 5135 bp in
f 100 bp
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AC108040/c
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Matches 201; Conserv
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2 (bases 1 to 163521)
Waterston,R.H.
Direct Submission
Submitted (24-JAN-2002) Genome Sequencing Center, Washington
                                                                                         1 (bases 1 to 163521)
Waterston, R.H.
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       AC108040.2 GI:18425316
ATG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                      Homo sapiens chromosome 4 clone SEQUENCE, 4 unordered pieces. ACLOSO40
                                                          The sequence of Homo sapiens 
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAACCCCGGTCTTTACTAAAAATACAAAAAAATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                  САЛАЛАСЛАСЛАСЛАЛАЛАЛАСЛАЛАЛАССАТАЛСА 355
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGAACCCGGGAGGTAGAGACTGCAGTGAGCCGAGACTGCGCCACTGCATGACAGAGCG 87310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGTGTGGTGCACACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGATGGAGAATCT
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/estimated_length=100

20529. .24488

/note="assembly_fragment"

24489. .24588

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/note="assembly_fragment"
33308. .33407
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39418. .39517
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28868. .28967
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73.1%;
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Pred. No. 1.8e-42;
0; Mismatches 74;
                                                                               clone
                                                                                                                                                                                                                                                                      DNA linear HTG 30-JAN-2002
RP11-210010, WORKING DRAFT
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                                                                            Query Match
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37 AAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAG 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 189000; agarose-fp
Insert size: 163221; sum-of-contigs
Quality coverage: 8.88 in Q20 bases; agarose-fp
Quality coverage: 8.85 in Q20 bases; sum-of-contigs
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On Jan 30, 2002 this sequence version replaced gi:18308830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_NH0210010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: submissions@watson.wustl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces
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89085
112703
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89085..112702
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88985. .89084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig25
clone_end:SP6
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/estimated_length=unknown
112803. .163521
                                                                                                                                                                                                                                                                                                                                                                                                     clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
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/chromosome="4"
                                                                                                                                                                        /note="assembly_name:Contig27"
                                                                                                                                                                                                                                                                    /note="assembly_name:Contig26"
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1664: gap of unknown length
8898: contig of 87320 bp in length
89084: gap of unknown length
112700: contig of 23618 bp in length
112802: gap of unknown length
163521: contig of 50719 bp in length.
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                                                                       39.2%;
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                                                 1; Mismatches
                                                                       Score 156.6; DB 12;
Pred. No. 1.9e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (Dases 1 to 196773) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-JAN-2003) Genome Center, University of Washington, Box 352145, Seattle, MA 98195, USA On Jan 29, 2003 this sequence version replaced gi:19310299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 196773)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 196773)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 3 clone RP11-755B10, AC114480
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Direct Submission
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HTG.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Sequencing vector: unknown; 3% of reads
Sequencing vector: plasmid; 97% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 19673b bases at least Q40
Consensus quality: 19675b bases at least Q30
Consensus quality: 196772 bases at least Q20
Insert size: 196773; sum-of-contigs
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                                                                                                                                                                                               Center project name: chr-3
Center clone name: RP11-755B10 (bc0671)
------Summary Statistics
                                                                                                                                                                                                                                                                                            Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                     Web site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                        Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                               Center: University of Washington Genome Center
                                                                                                                                                                                                                                                                         Project Information
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0, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rouse, G., Wu, Z., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 29-JAN-2003
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality Overlapping Sequences:
5': RP11-229A12 (UWGC:bc0315) AC092418, 11308-bp overlap
3': RP11-680P23 (UWGC:bc0527) AC099558, 118740-bp overlap This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file. Quality coverage: 8.4x in Q20 bases; sum-of-contigs SeqDerMap HindIII FngrPrnt <800 <800 SeqDerMap FngrPrnt zero Ś ORIGIN FEATURES Query Match
Best Local Similarity 71.4
Matches 222; Conservative source 37 AAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCCTGTAATCCCAG 96 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-755B10"
/clone_lib="RPCI human BAC library 1. .196773 Location/Qualifiers 39.2%; 71.4%; <800 <800 <800 <800 <800 <800 Score 156.6; DB 5; Length 196773; Pred. No. 2.1e-42; 1; Mismatches 80; Indels 8; ------<800 <800 <800 <800 <800 8; Gaps

SeqDerMap FngrPrnt

ECORI

<800

 Sequence Validation:

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VERSION
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AC016552/c
LOCUS
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                                                                                                                                                            Consensus quality: 92975 bases at least Q40
Consensus quality: 98251 bases at least Q20
Consensus quality: 100181 bases at least Q20
Consensus quality: 100181 bases at least Q20
Estimated insert size: 106000; pulse field gel estimation
Estimated insert size: 101858; sum-of-contigs estimation
Quality coverage: 5.46 in Q20 bases; pulse field gel estimation
Quality coverage: 5.69 in Q20 bases; pulse field gel estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 6, 2000 this sequence version replaced gi:7710241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Project Name: 294922
Center clone name: CIT-HSPC_285M15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Joint Genome Institute
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Homo sapiens chromosome 5 clone
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jnpublished
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is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ordered pieces.
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CTC-285M15, WORKING DRAFT
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DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 33
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                        Submitted (03-AUG-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 (bases 1 to 244525)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (06-DEC-2001) DOE Joint Genome Institute,
                                                                                                          2 (bases 1 to 244525)
DOE Joint Genome Institute.
                                                                                                                                                                        1 (bases 1 to 244525)
DOE Joint Genome Institute
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HTG.
                                                                                              Direct Submission
                                                                                                                                        Unpublished
                                                                                                                                                                                                         Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                   AC008499
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                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAAAAAACAAAACAAAACAAAAAAAAAGTAATAAGTGCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGAGACCAGCCTGGCCAACATAGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
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/clone lib="calTech human BAC library C"
63902. 64001
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/chromosome="5"
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76.6%;
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Ne 5 clone CTC-438O3, complete
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Pred. No. 1.8e-42;
L; Mismatches 62
                                                                                                                                                                         and Stanford
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                                                                                                                                                                         Human Genome Center
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A 94598, USA
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2 (bases 1 to 88848)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Garnd-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
                                                                                                                                                                                                                                                            1 (bases 1 to 88848)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone CTD-2314M10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 26, 2002 this sequence version replaced gi:17386226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 244525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome AC107377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: Phrap Quality >=40 99.7% of Sequence; Estimated Total Number of Errors is 0.4.
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC107377.4 GI:20377031
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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/mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="5"
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76.6%;

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Pred. No. 2.7e-42;
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17, clone
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Lamazares, R., Lianders, T., Lahoczky, J., Levine, R., Liau, G., MacChann, C., MacChann, M., Matchews, C., McCarthy, M., McEban, P., McKernan, K., McPheeters, M., McLiden, J., McReneu, L., MacChann, C., McCarthy, M., McEban, P., McKernan, K., McPheeters, M., McLiden, J., McReneu, L., McChan, P., McKernan, K., McPheeters, MayJor, J., Rapyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Norman, J., Rosetti, M., Strabauk, M., Riby, R., Riss, C., Bogov, P., Raman, J., Severy, P., Spancer, B., Schaper, S., Schauer, S., Scha
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------ Project Information
Center project name: L21459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
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complement(9022. .9328)
/rpt_family="""
                                                                                                                                                                                     complement (9849.
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complement(1891.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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        'rpt_family="AluJo"
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lement(8517. .866)
family="FRAM"
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_family="MIR"
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ement(5440
                          family="AluY"
5. .13997
                                                                       family="FRAM"
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Best Local Similarity
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ACI72796.2 GI:86203525
ACI72796.2 GI:86203525
HTGS_PHASE2; HTGS_DRAFT.
Callicebus moloch (Dusky titi)
Callicebus moloch
Callicebus moloch
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Primates; Platyrrhini;
Cebidae; Callicebinae; Callicebus.
1 (bases 1 to 187725)
Antonellis,A., Bass,D., Benjamin,B., Bera,J., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooke,S., Chu,G., Coleman,H.,
Franks,S., Fuksenko,T., Gestole,M., Greene,A., Guan,X., Gupta,J.,
                                                                                                                                                                                                                  AC172796
Callicebus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (18751...19065)
/rpt family="AluSx"
19095...19142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (18426. .18746)
/rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
complement(14478. .14608)
/rpt_family="FLAM_C"
14917. .14938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (17944. .18240)
/rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (17254. .1 /rpt_family="MER58A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14455. .14475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt
16519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="<30 Qual SNGL Region"
                                                                                                                                                                                                                  182725 bp
moloch clone LB5-41K3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="(A)n"
6. .15215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family="AluSx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 155.8; DB E
Pred. No. 2.7e-42;
0; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .17410)
                                                                                                                                                                                                                   DNA linear HTG 31-JAN-2006 WORKING DRAFT SEQUENCE, 9 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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                                                                                                                                                                                                                                                                                                                                               363
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AUTHORS
TITLE
* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 2543: contig of 22543 bp in length

* 22544 22643: gap of unknown length

* 22644 31875: contig of 9232 bp in length

* 31876 31975: gap of unknown length

* 31976 122998: contig of 91023 bp in length

* 123099 123098: gap of unknown length

* 123099 1336487: contig of 13389 bp in length

* 136488 136587: gap of unknown length

* 136488 136589: contig of 2782 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurson,N., Haghighi,P., Han,E., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G., Hurle,B., Idol,J.R., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies, E.H., Masiello,C., Maskeri,B., McDowell,J., Montemayor,C., Mullikin,J.C., Park,M., Prasad,A., Puri,O., Rantz,K., Reddix-Dugue,N., Sante,A., Schandler,K., Schueler,M.G., Sison,C., Stantripop,S., Taye,A., Thomas,J.W., Thomas,P.J., Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Withers,T.R., Young,A. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the sequence assembly is generally based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-JAN-2006) NIH Intramural Sequencing Center, ! Fishers Lane, Rockville, MD 20852, USA On Jan 31, 2006 this sequence version replaced gi:82617757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-NOV-2005) NIH Intramural Sequencing Center, 5625 Fishers Lane, Rockville, MD 20852, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 182725)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.9909 Consensus quality: 179767 bases at least Q40 Consensus quality: 180990 bases at least Q30 Consensus quality; 181586 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: mrn
Center clone name: 041K03
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Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: NIH Intramural Sequencing Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 9.44x in Q20 bases; a Quality coverage: 11.11x in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 214000; agarose-fp
Insert size: 181925; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- Project Information

    Summary Statistics

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141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC

200 23389

TAGAGACCAGCTTGGCCAACATGGTGAAAACCTCGTCTACTAAAAAATACAGGAATTAGC

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                                                                       Matches 225;
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 gap
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                                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
 ACGCCTGTAATCCCCAGCACTTTGGGAGGCTGAGATGGGTGAATCACCTGAGGTCAGAAGT 23449
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139470
148609
148709
157276
157376
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                                                                         Conservative
                                                                                                                                                               /note="assembly_fragment
clone_end:SP6
vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50743. .182725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="clone overlaps with GenBank Accession Number AC174418 clone LB5-285122 (center project name mrm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment
missing T7 clone end on 5' end of insert'
                                                                                                                                                                                                                           179902. .18272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /estimated_length=unknown
123099. .136487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="clone overlaps with GenBank Accession Number
AC172795 clone LB5-290P9 (center project name mro)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Callicebus m
/mol_type≃"genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                            148709. .15727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
139370. .139469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
136488. .136587
/estimated_length=unknown
136588. .139369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
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31976. .122998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="BAC resource: http://bacpac.chori.org/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="LB5-41K3"
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                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment"
48609. .148708
                                                                                                                                                                                                                                                                                                                                                                                                                                                 39470. .148608
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                                                                                                                                                                                                                                                                      note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                       estimated_length=unknown
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148608: contig of 9139 bp in length
148708: gap of unknown length
157275: contig of 8567 bp in length
157375: gap of unknown length
179801: contig of 22426 bp in length
179901: gap of unknown length
182725: contig of 2824 bp in length.
                                                                                                                                                                                                                                                              79802. .179901
                                                                                                                                                                                                                                                                                                                  estimated
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                                                                                          39.0%;
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                                                                                                                                                                                                                                                                                                                  _length=unknown
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                                                                         Score 155.8; DB 12,
Pred. No. 3.9e-42;
1; Mismatches 83;
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                                                                                                           DB 12; Length 182725;
                                                                             Indels
                                                                           10; Gaps
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RESULT 36
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-NOV-1998) Department of Molecular Biotechnology, Boy 357730 University of Washington, Seattle, Washington 98195, USA Sequencing methodology: high redundancy shotgun using plasmids. Interspersed Repeats were identified with RepeatMasker (available from http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216387 bp DNA linear PRI 23-DEC-1998 Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds. AF109907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rowen,L., Madan,A., Qin,S., Abbasi,N., Dors,M., Madan,A., Dickhoff,R., Shaffer,T., James,R., La: Complete sequence of the gene for presentin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                  oin(<1465. .1522,5979. .6139,14890. .15075,17363. .17416,
17550. .17733,21177. .22463,23822. .24044,24159. .24248,
25789. .25862,27305. .27455,28794. .29118,29491. .29765,
30115. .30213,32250. .32297,37674. .>37766)
                                                                 join(<1465. .1522,5979. .6139,14890. .15075,17363. .17416, 17650. .17733,21177. .21463,23822. .24044,24159. .24248, 25789. .25862,27305. .27455,28794. .29118,2991. .29765, 30115. .30213,32250. .32297,37674. .37766)
//notee "unknown; intron-exon boundaries defined by ESTs A1247672, AA677761, T40389, AA64648, AA147425, AA677761, T40389, AA64644, AA170655, and cDNA in 140392; the sequence in 140392 begins at 28812; the exons from 21177-21463 and 23822-24044 contain a repeat, only 1 EST, T40380 markhas and 23822-24044 contain a repeat, only 1 EST,
T40389 matches the exon from 21177-21463; since several ESTs end in the beginning of this exon, and several 5' ESTs start at the end of this exon, it is possible that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="genomic DNA"
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Lasky,S. and Hood,L.
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complement(9200...9400)
/rpt_famil...
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/rpt_family="Aluy"
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/rpt family="FLAM_C"
complement (11506 . .11784)
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SNS PGQPNSVEKKKLPVSVENK FEDEDSDDVPKRRKLVPLDYGEDDKNATKGTVNTE
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VDFVCSKYMAHSSPGSILDDYAMVLDEEAEV FI VKMWRLLLI VETEAKKIGLVK"
  /note="sequence could be aacgg--possible compression"
complement(12658. .12788)
                                                                                                                        complement (11928.
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complement(10572. .1
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complement(7334. .763
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complement(2992. .3
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GEKKLLVKVDAKTKAQLDEWKAKKKASNGNARPETVTNDDEEALDEETKRRDQMIKGA
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|db_xref="GI:4050087"
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22297. .27
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23832.
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complement(22333...22
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21225.
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complement(16115...16401)
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 /rpt_unit_seq="gaa"
complement(30243. .30267)
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/rpt_family="AluJo"
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plement(27846...28147)
t_family=""..."
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t_family="AluSg"
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t_family="POLY_A"
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family="AluY"
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ement (2000)
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ement (2011)
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ement(26177
                                     family="AluSx"
                                              ement (28394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .21305
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RESULT 37 AL732374/c VERSION KEYWORDS Ô 망 Ś 밁 Ş 문 á 밁 S REFERENCE SOURCE COMMENT DEFINITION ACCESSION Pocus Query Match Best Local Similarity Matches 218; Conserv AUTHORS TITLE ORGANISM JOURNAL 195538 195778 195658 Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 2, 2002 this sequence version replaced gi:23393869. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX 141 201 81 Human DNA sequence from clone RP13-444K19 on chromosome X Contains a mitochondrial ribosomal protein S18C (MRP518C) pseudogene, the 3' end of the gene for a novel protein similar to PHD finger protein 2 PHF2 and a CpG island, complete sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest. Web site: http://www.sanger.ac.uk Contact: vega@sanger.ac.uk Center: Wellcome Trust Sanger Institute Center code: SC Direct Submission Homo sapiens AL732374.14 GI:23476649 HTG; CpG island; MRPS18C; PHF2. http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6 of Pieter de Jong. For further details RP13-444K19 is from the library RPCI-13.2 Hominidae; Homo. Eukaryota; Metazoa; Homo sapiens (human) Mammalia; Eutheria; CTTGAACCTGAGAGGCAGAGGGTGCAGTGAACCAAGATACTCCAGCCTAGTGACACAGCG 195777 ATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTCAAGAGA TCGAGACTATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGC 195657 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA AGACKCCGTCTCAAAAAACAACAACAAAAAAAACAAAAAAAACCATA 352 AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGAT----CACAGAGTGAGCAGAGTG 309 TGGGCGTGGTGGTATGCATCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAGTTG 195717 TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGA------GCCGGAGATTGC 253 (bases 1 to 224187) Conservative 39.0%; 77.0%; Genome Center Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; 1; Mismatches Score 155.8; DB 5 Pred. No. 4.2e-42; 5 see constructed Indels Length 216387; by the group 140 195597 2

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mRNA
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="RPCI-13.2"
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ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGEN WAY I SLEF SU KLEMWYELFAN YN DE TRANSPORTER TO THE MEGNES SENOMERFOLOVED BYTTDFHI DEGGTSWAYNULKGEK IF YLI REPINALITIEGUASS.SSNOMERFOLOVED KCYKCSVKQGQTLFI PTGWIHAVLTPVDCLAFGGNFLHSLNI EMQLKAYEI EKRLSTA DLFREPNFETI CWYVCKHILDI FRGLERNRHPASYLVHGGKALILAFRAWTRKEALF DHEDEI PETVRTVQLI KDLAREIRLEDI FQUNGKTSNI IFGLORI FGAGSI PLTRPA HSTSVBMSRLSLEPSKNGSKKKGLKPKELFKKAEKKGKESSALGPAGQLSYNLMDTYSH HSTSVBMSRLSLEPSKNGSKKKGLKPKELFKKAEKKGKESSALGPAGQLSYNLMDTYSH QALKTGSFQKAKFNI TGACLMDSDDDS DELDLDGNESPLALLAFAGQUSTKRVKSLSKSR RTKI AKTONKARLAMAEQVMEDETDLDSDDELDLDGNESPLALLAFARI I I RFKF PKLPRAK PCSDDNRVREBGCVERDI EBDYTTDEDDMYEGVEGKLGNGSGAGGILDLLKASRQVGED RYAALTEAPASPSTOEAI QGMLCMANILQSSSSPATSSLQAMWTGGQDRSSGSSSGI
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.181447),
.178504),
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RESULT 38
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 САЛАЛАСЛАСЛАСАЛАЛАЛАСАЛАЛА 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                    chromosome 6, constructed by the Sanger Centre Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                     On Nov 7, 1999 this sequence version replaced gi:6165363.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA sequence from clone RP1-193N7
Contains the 5' end of the MANIA1 gene
class 1A, member 1 (Man9-mannosidase (N
                                                                                                                                                                                                                                                                                                                                                                      Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
    Center:
                                           VECTOR: PCYPAC2
                                                                   Pieter de Jong. For further deta
http://www.chori.org/bacpac/home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mannosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL078600.15 GI:6273536
HTG; CpG island; HUMM9; MAN1A1; MAN9; Man9-mannosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSJ193N13
                                                                                                              RP1-193N13 is from the library RPCI-1 constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
1 (bases 1 to 122961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGATCGCACCACCGCACTCCAGCCTGGGTGACAGAGCAAGACTTCATCTCAAAAAAATA 43946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAAATAAAAATAAAATAAATA 43920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
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Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join(128280 ...129067,129799 ...129908, 148509 ...146604,170579 ...170892,171481 ...171614, 172743 ...172828,173431 ...173609,178401 ...178504, 179266 ...179568,181358 ...181447,185535 ...185626,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDDDDPALKSRPKKKKNSDDAPWSPKARVTPTLPKQDRPVREGTRVASIETGLAAAAA KLAQQELQKAQKKKYIKKKEPLLKEVEQPRPQDSNLSLTVPAPTVAATPQLVTSSSPLP PPEPKQEALSGSLADHEYTARPNAFGNAQANRSTTPMAPGVFLTQRRPSVGSQSNQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGKRPKKGLATAKQRLGRILKIHRNGKLLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTVSNSPASQRTPGKRPIKRPAYWRTESEEEEENASLDEQDSLGACFKDAEYIYPSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.9%;
74.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ce from clone RP1-193N13 on chromosome 6q21-22.31 end of the MAN1A1 gene for mannosidase, alpha, 1 (Man9-mannosidase (MAN9), HUMM9). Contains a CpG
                                                                                             further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,
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Pred. No. 5e-
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5e-42;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
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AL135738 AL673800 AU119410 AU135696 AV650705 AV689108
AV701374 BE003222 BE815845 BE877565 BC428373 BC548683
BI441201 BI964041 BI964247 BM538709 BM806736 BM933828
match: cDNAs: AF027156 AK025599 U03457 U03458 U04299
U04301 X74837 Y12503"
/db_xref="HSSP:1F03"
/db_xref="HSSP:1F03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MANIA1"
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/standard_name="OTTHUMP00000017107"
/note="maTch: proteins: AAH15265 CE08947 002773 060476
/note="maTch: proteins: AAH15265 CE08947 002773 060476
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/clone="RP1-193N13"
/clone_lib="RPCI-1"
                                                                                                                                                                                                                                      /proteIn id="CAB75695.2"
/db_xref="GI:56203652"
/db_xref="GOA:P33908"
/db_xref="HGOA:P33908"
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join(complement(5197...
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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MO 63108, US
5 (bases 1
Waterston, R.
                                              Direct Submission
Submitted (24-MAR-1999) Genome
University School of Medicine,
                                                                                              4 (bases 1 to 126462)
Waterston, R.H.
                                                                                                                                               Submitted (12-JUN-1998) Genome University School of Medicine,
                                                                                                                                                                                               3 (bases 1 to 126462) Waterston, R.H.
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Genome Res. 8 (11), 1097-1108 (
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Sulston, J.E. and Waterston, R.
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SVPEVNIRFVGGLLSAYYLSGBEIFRKKAVELGVKLLPAFHTPSGIPWALLNMKSGIG
RNWPMASGGSSILAEFGTLHLEFWHLSHLSGNPIFAEKVMNIRTVLNKLEKPQGIYPN
YLNPSSGQWGGHHVSVGGLGDSFFSYLLKAWLMSDKTDLEAKKMYFDAVQAIETHLIR
KSSSGLTYIAEWKGGLLEHKMGHLTCFAGGMFALGADAAPEGWAQHYLELGAEIARTC
HESYNRTFMKLGPEAFRFDGGVEAIATRQNEKYYILRPEVMETYMYMWRLTHDPKYRK
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Pred. No. 4.4e
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                                                                                                                                                     Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 24, 1999 this sequence version replaced gi:3213121.
                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (28-JUL-1999)
                                                                                                                                                                                                                                                 Waterston, R.
                                                                                                                                                                                                                                                                      University, 4444 Forest 6 (bases 1 to 126462)
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_DJ0747G18
                                                                Web site: http://genome.wustl.
                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                             Submission
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lone. It may be shorter because we only sequence overlapping lone sections once, or longer because we provide a small over neighboring This sequence may not represent the entire insert of this data submissions. overlap

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless all regions were double stranded, sequenced v restriction digest. otherwise noted:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/pIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc MAPPING INFORMATION: and

This clone was derived from human PAC library RPCI-4, prepared pieter de Jong and coworkers at the Roswell Park Cancer Instit (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is SOURCE INFORMATION: prepared by Institute 18

one male donor.

The clone may be obtained either from Genome Systems, (http://www.resgenomesystems.com) or Research Genetics, 1 (http://www.resgen.com); or from Pieter de Jong.

VECTOR: PCYPAC2
VECTOR: DETABLE INFORMATION:
NEIGHBORING SEQUENCE INFORMATION:
ACTUAL START Of this clone is at base position 1 of actual end is at 126462 of RP4-747G18.

RP4-747G18;

jot correct. submitted assembly double stranding from 79862 to 80357 in the PAC RP4-747G18 can be guaranteed although their sequence fidelity is believed to nteed although their sequence fidelit Digests using EcorV and HindIII are

FEATURES repeat_region repeat_region repeat_region /rpt_ 1238. /rpt_family="Alu" 578. ...898 organism="Homo sapiens" clone_ clone="RP4-747G18" map="7g22-31.1" chromosome="7" db_xref="taxon:9606" ocation/Qualifiers, .126462 _family="Alu" . .1373 type="genomic _lib="RPCI-4"

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                                        2 (bases 1 to 132492)
Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L. Direct Submission
Submitted (20-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                               1 (bases 1 to 132492)
DOE Joint Genome Institute, Stanford
Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                 ACUU7616 132492 bp DNA linear PRI 18-DEC-2003 Homo sapiens chromosome 16 clone RPI1-547D14, complete sequence.
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                        AC007616.5
                                                                                                                                                                                                                             Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAACAATAACAAAAAAAAAAACAAGTGCAAGGTCTTGCCTTTGAGTTGGGGTCAGA 93960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAAACAACAACAAAAAAAAAAAAAACCATAAGACATTGTCCATCTGCGGTTCCCAGA 379
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/rpt_family="Alu"
13905. .14214
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16479. .16579
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5202. .15380
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Pred. No. 4.5e-42;
1; Mismatches 72;
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AUTHORS
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A¢027249/c
                                                                                                                                                                                                             ACCESSION
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Matches 198;
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                                                                                                                                                                                                           SEQUENCE,
AC027249
                                                                                                                                                                                                                          AC027249 145679 bp DNA linear Homo sapiens chromosome 11 clone RP11-753E7 map 11, SEQUENCE, 35 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-DEC-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 18, 2003 this sequence version replaced gi:21700556.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is not the entire sequence of the clone (entire sequence 168.9kb). It is clipped at the overlap with AC007613. The number of bases overlapped is 29296.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
                                                                   Hominidae;
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                             Homo sapiens
                                                                                                                                                                                    AC027249.2 GI:7651924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanford Human Genome Center and Los Alamos National Laboratory. DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-JUL-2002) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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                                                                               lammalia; Eutheria; Euarchontoglires; Primates;
    (bases 1 to 145679)
irren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                        AAAACAAAACAAAACCAAAAACTAAA 19470
                                                                                                                                                                                                                                                                                                                                                                                                            AAAACAACAACAAAAAACAAAAAAACCATAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCTGGTGGCATGCGCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCT
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                                                                                                                                          HTGS_PHASE1; HTGS_DRAFT sapiens (human)
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mol_type="genomic DNA"
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chromosome="16"
                                                                 Homo.
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Pred. No. 4.6
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                                                                                   Catarrhini;
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WORKING DRAFT
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A 94598, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA On Apr 27, 2000 this sequence version replaced gi:7331619. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------Project Information
Center project name: L8860
Center clone name: 753_E_7
                                                                                                                                                             3865
                       11580:
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gap of
contig
gap of
contig
                                                                             gap of contig
                                                                                                                     gap of contig
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Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C.; Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Weneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teffaye, S., Theodore, J., Tirrell, A., Tarvers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Direct Submission Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H. Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F. Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Cc. Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Diak, Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Diak, K., Dewar, M., Dewar, K., Dewar, M., Dewar, M., Dewar, M., Dewar, M., Dewar, M., De Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Abraham, H., Allen, N., Beda, F., Collins, S.,

Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR Research

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 129416 bases at least Q40
Consensus quality: 137400 bases at least Q30
Consensus quality: 137400 bases at least Q20
Consensus quality: 140385 bases at least Q20
Insert size: 154000; agarose-fp
Insert size: 142279; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; sgarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs agarose-fp sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. contig of 1125 bp in 1 gap of 100 bp in 1 gap of 100 bp in 1 gap of 100 bp in 1 contig of 1338 bp in 1 gap of 100 bp in 1 gap of 100 bp in 1 gap of 105 bp in 1 f 100 bp g of 2058 bp in l f 100 bp g of 2303 bp in l f 100 bp 100 bp of 1696 bp ä length length length length length length

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2527. .3864
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/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                'map="11"
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3: gap of 100 bp
5: gap of 100 bp
2: contig of 9392 bp in length
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2: contig of 8137 bp in length
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6: contig of 7283 bp in length
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8: contig of 7763 bp in length
8: gap of 100 bp
8: contig of 8570 bp in length
8: gap of 100 bp
8: contig of 8570 bp in length
8: gap of 100 bp
9: contig of 8250 bp in length
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9: contig of 8250 bp in length
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9: contig of 13611 bp in length.
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                                      APO01024 183444 bp DI
Homo sapiens genomic DNA, chromosome
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                                                                                                                                                                                                      TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG-CAGAGTGAGACKCCGTC 319
                                                                                                                                                                                                                                                  TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC 260
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24136. .26117
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5324. .7019
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Pred. No. 4.8e-42;
1; Mismatches 62
                                          DNA linear PRI 02-JUL-2003
ne 11 clone:RP11-832N8, complete
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
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AUTHORS
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                                                                                                                                                                                               202138 bp DNA linear
Homo sapiens chromosome 11 clone RP11-531E6 map 11,
SEQUENCE, 22 unordered pieces.
AC018423
                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-531E6
                                                                                                         Eukaryota; Metazoa;
                                                                                                                              Homo sapiens
                                                                                                                                                               AC018423.4 GI:10045404
HTG; HTGS_PHASE1; HTGS_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@goc.riken.go.jp/, VILI:hattori@goc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jul 1, 2003 this sequence version replaced gi:31790714.
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Homo sapiens
                                                                      Hominidae; Homo
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                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO
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blished Only in Database (2000)
(bases 1 to 183444)
                                                 (bases 1 to 202138)
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/mol_type="genomic DNA"
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                                                                                    Chordata; Craniata;
Euarchontoglires; Pi
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Totoki, Y.,
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Pred. No. 5.4
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nes 62;
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                                                                                        Primates;
                                                                                                         Vertebrata; Euteleostomi;
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                                                                                        Catarrhini;
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Baguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Colling, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Feaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Mardrim, J., Morrow, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 9, 2000 this sequence version replaced gi:6649385. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: L3744

Center clone name: 531 E 6

Center clone name: 531 E 6

Sequencing vector: M13, M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 188769 bases at least Q30
Consensus quality: 195790 bases at least Q30
Consensus quality: 19659 bases at least Q20
Insert size: 210000; agarose-fp
Insert size: 210000; agarose-fp
Quality coverage: 4.4 in Q20 bases; sgarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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96732: contig of 6316 bp in length
96833: gap of 100 bp
106557: contig of 9725 bp in length
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155574: gap of 100 bp
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193976: gap of 100 bp
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LOCUS DEFINITION ACCESSION RESULT 44 AC099489

AC099489 204493 bp DNA linear PRI 04-FEB-Homo sapiens chromosome 16 clone CTD-3088G3, complete sequence. AC099489

PRI 04-FEB-2003

VERSION KEYWORDS

AC099489.2 GI:28201477 HTG. Homo sapiens (human)

SOURCE

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102122 TCAAAAAAAAAAAAAAAAAAAGGAGAA 102096
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                                                                                                                 TGGGTGTGGTGGCCCACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGACAGGAGAATCG 102183
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                                                                                                                                    TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
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RESULT 45
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AL355388
Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
NOTE: Shatter libraries failed to verify the dinucleotide repeat
region 65514-65789. Unsure number of repeat copies 65514-65789.
Forced join at 65675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-FEB-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 4, 2003 this sequence version replaced gi:16930905.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-NOV-2001) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA (Dases 1 to 204493)

DOE Joint Genome Institute, Stanford Human Genome Center
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National Laboratory
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Alamos National Laboratory.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ww-shgc.stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                              GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
                                                                                                                                                                                       TGAACCCAGGAGGAGGGAGAATTGCTTGAACCCTGGGCGACAGAGGCGAGACTCCATCTCA
                                                                                                                                                                                                                                                                                                                                          GAGACCAGCCTGGCCAACACGGTGAAACCCCCAACTCTCCTAATAATAAAAAAATTAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTGTAATCCCAGCACTTGGGGAGGCCAAGGCGGGTGGATCACTTGAGGTCAGGAGTTT
                                                                                                                                                 ААААСААСААСАААААААССАТАА 353
                                                                                                                                                                                                                            AGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCA 322
                                                                                                                                                                                                                                                                 GGCCTGGTGGCATGCGCCTGCAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCT 14658
                                                                                                                                                                                                                                                                                                     GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                AAAACAAAACAAAACCAAAAACTAAA 14749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
388 205463 bp DNA linear PRI
DNA sequence from clone RP11-336K24 on chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="NOTE: Shatter libraries failed to verify the dinucleotide repeat region 65514-65789. Unsure numi repeat copies 65514-65789. Forced join at 65675."
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/chromosome="16"
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73.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 155.4; DB 5
Pred. No. 5.7e-42;
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AUTHORS
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JOURNAL
                                                                      gene
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                                                                                                                                                                                                                          gene
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Clone requests: clonerequest@sanger.ac.uk
On Mar 29, 2003 this sequence version replaced gi:28446036.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 5' end of the RIT1 gene for Ras-like without CAAX 1, the gene for a novel protein (KIAA0907), the ARHGEF2 gene for rho/rac guanine nucleotide exchange factor (GEP) 2, four novel genes, the SSR2 gene for signal sequence receptor beta (translocon-associated protein beta), the Clorf6 gene for chromosome 1 open reading frame 6, the gene for mitogen-activated protein-binding protein-interacting protein (MARBEFP), the RAB25 gene for RAB25 (member RAS oncogene family), the 5' end of the LMNA gene for lamin A/C and three CpG islands, complete sequence.
Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                     http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                               RP11-336K24 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
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HTG; ARHGEF2; Clorf6; KIAA0907; LMNA; MAPBPIP; RAB25; RIT1; SSR2.
                                                                                      Center code: SC
                                                                                                                        Center: Wellcome Trust Sanger Institute
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1 (bases 1 to 205463)
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                                                                                                                                                                   Genome Center
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                                                                                                                                                                                                                                                                                                                              by the group
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers

1. 205463

/organism="Homo sapiens"

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gene
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/db_xref="GOA:Q5VY89"
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complement (AL139128.24:141244. .141317),
complement (AL139128.24:141116. .141123),
complement (AL139128.24:1411824. .141015),
complement (AL139128.24:136911. .137131))
/gene="RITI"
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complement(AL139128.24:140824..141015),
complement(AL139128.24:136911..137131))
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complement (AL139128.24:136787. .137131))
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/protein_id="CAH72622.1"
/db_xref="GI:55663544"
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/produc_t="Ras_like without CAAX 1"
/note="match: ESTS: Em:BF185015.1 Em:BF208489.1
match: CDNAs: Em:AF084462.1 Em:U71203.1 Em:U78165.1
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note="match: ESTs: Em:BE782613.1"
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note="match: ESTs: Em:BQ918446.1"
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                                                                                                                                                                                       TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                     TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
TGCTTGAACCCGGGAGGCGGAAGTTGCAGTGAGTCTAGATCGCAGAGTGAGACTCCGTCC 177456
                                            TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                              CGAGCATGGTGGCAGACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGACAG--GAGAAT 177396
                                                                                                                                                                                                                                                                                        TCGAGACCAGCCTGACCAACAAGGTGAAACCTCGTCTCTACTAAAAATACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Jocus tag="RP11-336K24.1-001"
/Jocus tag="RP11-336K24.1-001"
/Jocus tag="RP11-336K24.1-001"
/Jocus tag="RP11-356K24.1-10598,17307..1
15055..15308,15541..15598,17307..1
20356..20519,20784..20879))
/gene="RP11-336K24.1-003"
/Jocus tag="RP11-336K24.1-003"
/Jocus tag="RP11-336K24.1-1003"

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complement (join (6723 . 8000, 9553 .

11179 . 11352,15055 . 15308,15541.

19312 . 19523,20356 . 20519,20784.

23392 . 23520,27313 . 27529,28016 .

/gene="RP11-336K24.1"
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/note="match: cDNAs: Em:/
complement(6725)
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Em:BC006621.1 Em:BC062637.1"
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RFPEDHDPTIEDAYKLRIRIDEPANLDILDTAGQAEFTANDQYMRAGEGFIICYSI
TDRRSGFHEVREFKQLIYAVRRTDDTFYVLVGWKSDLKQLRQVTKEEGLALAREFSCPE
FETSAAYRYYIDDVFHALVREIRRKEKEAVLAMEKKSKPKNSVWKRLKSPFRKKKDSV
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/product="novel protein"
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/db_xref="GI:55663543"
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/locus_tag="RP11-336K24.1-003"
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/locus_tag="RP11-336K
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/db_xref="InterPro:IPR005225"
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74.7%;
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Pred. No. 5.7e-42;
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.23055,23392.
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.20836,22976. .23055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 18, 2003 this sequence version replaced gi:18057078.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US 4 (bases 1 to 116130)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: Phrap Quality >=40 100% of Estimated Total Number of Errors is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAR-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Finishing Completed at Stanford Human Genome Center and Los Alamos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www.jgi.doe.gov
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DOE Joint Genome Institute.
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DOE Joint Genome Institute,
Alamos National Laboratory.
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AC026423.9 GI:29029225
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                              Similarity
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TGAGATCGCAGAGTGAGCCGAAATCACAGAT------CACAGAGTGAGAGTGAGAC
                                                       CGGGCTTGGTGGCATGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGGAAGGT 11486
                                                                                     TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                              TCGAGACCAGCCTGGCCAACATGGTGAGACCTCATCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
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Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo gapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                         clone="CTD-2169M19"
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Pred. No. 5.1e-42;
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18 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bubay, C., Burch, P., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Bydn, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, J., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Foster, P., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falla, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Guevara, W., Gunarathe, P., Hable, S., Harris, K., Harr
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Direct Submission
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Baylor Plaza, Houston, 3 (bases 1 to 177640) Worley, K.C.
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Homo sapiens 12 BAC RP11-206B11 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                            local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not
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Submitted (30-SEP-2001) Human Genome Sequencing of Molecular and Human Genetics, Baylor College of Plaza. Houston, TX 77030, USA
                                                                                                                                                                       SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are of sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones.
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OVALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Oct 22, 2002 this sequence version replaced gi:15809129 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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FEATURES

Location/Qualifiers

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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complement(11325. .11)
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complement(5123.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              family="(TTA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _family="L1M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _family="MLT1C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="L1MB2"
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                                                                                                                                              family="LTR33"
                                                                                                                                                                                                                                                                                                             _family="MER102"
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 38.8%;
73.7%;
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ement (2001)
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                                                                                                     _family="MLT1J2"
                                                                                                                                 family="AluSx"
                                                                                                                                                                                   family="(TTCA)n"
                                                                                                                                                                                                          family="L1PA13"
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                                                                                                                                                                                                                                                                                         family="AluSx"
                                                                                                                                                                                                                                                                                                                                          family="L1MC2"
                                                                                                                                                                                                                                                                                                                                                                     family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                               family="(TTTTG)n"
                                                                                                                    .14811
                                        .17120
 Score 155.2; DB 5
Pred. No. 6.2e-42;
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            DB 5;
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                                                                                                                                                                                                                                                                                                                                                                  Young,G., Zainoun,J., Zainmer,...

Proving,G., Zainoun,J., Zainmer,...

Direct Submission

Submitted (12-MAY-2000) Whitehead Institute/MIT Center for Genome Submitted (12-MAY-2000) Whitehead Institute/MIT Center for Genome Submitted (12-MAY-2000) Whitehead Institute, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 7, 2000 this sequence version replaced gi:8671969.

All repeats were identified using RepeatMasker:

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boughlavkiy, L., Boukhgalter, B., Erown, A., Burkett, G., Collins, S., Coguslavkiy, L., Boukhgalter, B., Erown, A., Burkett, Collins, S., Collymore, A., Coake, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreita, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Kaland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Laborne, K., Laborne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178079 bp DNA linear Homo sapiens chromosome 1 clone RP11-206C14 map 1, SEQUENCE, 11 unordered pieces.
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Birren,B., Linton,L., Nusbaum,C. and Lander,B.
Homo sapiens chromosome 1, clone RP11-206C14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Center project name: L7679
Center clone name: 206 C 14
----- Summary Statistics
Sequencing vector: M13; M77815; 42% of reads
Sequencing vector: Plasmid; n/a; 58% of reads
                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
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8649. .9685
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                                                                                                                  /estimated
22787. .34
                                                                                                                                                                                                                                                                   14638.
                                         /note="assembly_fragment"
34298. .34397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
11208. .11307
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                                                                                                                                                                                                                                                                                                                                    4538. .14637
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Insert size: 170000; agarose-fp
Insert size: 177079; sum-of-contigs
Quality coverage: 6.2 in Q20 bases; agarose-fp
Quality coverage: 5.9 in Q20 b.

NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 172732 bases at least Q40 Consensus quality: 175502 bases at least Q30 Consensus quality: 176567 bases at least Q20
organism="Homo sapiens"
                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130369 CTTGAACCCAGGAGGCGGAGGTGACAGAGCGAGCCTGGGTGATAGAGCAATACTTCATCT 130310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 TCGAGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAAATACAAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGGGGGATCACCTGAGGTCAAGAGA 140
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:12831806.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EWBL; Sw:, SWISSPROT; Tr:, TREWBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       ALI62384 68465 bp DNA linear PRI 18-MAY-200 Human DNA sequence from clone RPI1-21817 on chromosome 9 Contains novel gene similar to RAN binding protein 6 (RANBP6), the 5' end of a novel gene, a novel gene and a CpG island, complete sequence.
                                                                                                                                                                                                                   Tracey,A.
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             AL162384.14 GI:13274331
HTG; CpG island; RANBP6.
                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCTCTGGTGACTCACACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGG 130370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAAACAAAACAAAACAAAACAAAA 130284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAACTACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGAAAGGTGGATCACCTGAGGTCAGGAGT 130490
                                                                                                                                                                                                                                  (bases 1 to 68465)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47851. .47950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /estimated_len
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment
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8079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 155.2; DB 1
Pred. No. 6.2e-42;
1; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 178079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRI 18-MAY-2005
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-21817 is from the library RPCI-11.1 constructed by the group of pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //www.chori.org/bacpac/home.htm
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BM677000.1 BM799977.1 BM800655.1 BQ001465.1 BQ068431.1

BQ2271775.1 BQ220742.1 BG653718.1 BQ722086.1

match: CDNAs: AF039023.1 AF294327.1 AK001982.1 AK017701.1

BC001497.1 BC012805.1 BC019309.1 BC019838.1 BC020012.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(complement(3518. .4059), complement(AL353606.12:14362. .14562)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(complement(3518. .4059),
complement(AL353606.12:14362. .14562),
complement(AL365360.9:149198. .150476))
                                                                                                                                                                                                                                                                                                               Q96E78 Q9EQ30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (7366)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC026487.1 U72761.1 Y08890.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Clone_left_end: RP11-21817"
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                                                                                                                                                                                                                                                                                                                                           standard name="OTTHUMP00000021039"
note="match: proteins: AAH01497 AAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     locus_tag="RP11-546N22.5-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="RP11-21817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Center
                                                                                                                                                                                                                                                                                      start=1
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RESULT 50
AC068889
LOCUS
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     AC068889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAAGACCAGCCTGACCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCGGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                      CTTGAACCCGGGAGGTAGAGACTGCAGTGAGCCGAGACTGCGCCACTGCATGACAGAGCG 24050
                                                                                                                                                                                                                                                                                                              TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                 AGACKCCGTCTCAAAAACAACAACAAAAAAAACAAAA 344
                                                                                                                                                                                                                                                                                                                                                                   TGGGTGTGGTGGCACACGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGATGGAGAATCT 23990
                                                                                                                                            AGACACCATCTCAAAAAAAAAAAAAAAAAAAAAAGGAA 24085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Clone_right_end: RP11-165014"

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NHPVVIGPNNSNLPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLECVS
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IGEGCHQQMESILDETVNSVLLFLQDPHBFVRAAASTTTLGQMATDPAPNFQKKFHETV
IAALLRTMENGGNQRVGSHAASALIFFIEDCPKSLLVLYVDSNVKNLHSVLVLVLVLGLEI
IRNGTKLALEQLVTTIASVADTIEEKFVPYYDIFMPSLKHIVELAVQKELKLLRGKTI
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/locus_tag="RP11-218I7.1-002"</pre>
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/db_xref="Uniterpro:IPR000357"
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/translation="MKISQDPHPRVEABACTTLGQMATDFAPNFQKKFHETVIAALLR
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/proteIn_id="CAI12714.1"
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                                                                                                                                                                                                                                                                                                                Submitted (01-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                            Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
[bases 1 to 73433]
                                                                                                                                                                                           Submitted (11-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                        2 (bases 1 to 73433)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Balarbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryshine,C., Burrell,K.L., Byrd,N.C.
                                                 Direct Submission
                                                                Worley, K.C.
                                                                                                                                                             Worley, K.C.
                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeats are identified using RepeatMasker (A. Smit and P. G. unpublished.) for Human and Mouse sequences.

Genes and Region of sequences similarity are identified by BI (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to t EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-
of a local database that includes entries from dbSTS,
local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
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915._.1149
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                                      ВP
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07-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

26-JUL-2000

14-AUG-2000

16-AUG-2000

17-AUG-2000

18-AUG-2000

19-AUG-2000

19-AUG-2000

19-AUG-2000

10-SEP-2000

11-SEP-2000

11-SEP-2000
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds. 07-NOV-2001 (first entry) immune/haematopoietic antigen genomic sequence SEQ ID NO:38713.

Homo sapiens.

WO200157182-A2

17-JAN-2001; 2001WO-US001354

02-MAR-2000; 31-JAN-2000; 04-FEB-2000; 2000US-0179065P. 2000US-0180628P. 2000US-0184664P. 2000US-0186350P

19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000 17-MAR-2000; 18-APR-2000;

2000US-019974P.
2000US-0199173P.
2000US-0199173P.
2000US-02194867P.
2000US-02148867P.
2000US-0214887P.
2000US-0211489P.
2000US-0211899P.
2000US-021899P.
2000US-0224519P.
2000US-0225213P.
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14-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 02-OCT-2000

metastasis.

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2000US-0236370P.
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2000US-023703P.
2000US-0237039P.
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2000US-0237040P.
2000US-0237040P.
2000US-0241785P.
2000US-0241808P.
2000US-0246475P.
2000US-0246477P.
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2000US-0246528P.
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2000US-0236369P.
    RESULT 4
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AC AAK87161;
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Best Local S
Matches 201
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08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16163 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483426/52
    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer.
                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41973.
                                                                                               07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAA 195
                                                                                                                                                                                  standard; DNA; 16163
                                                                                                                                                                                                                                                                                                    GGAAAAAAAAAAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                      TGAGCCGAAACTGCACCACTACACTCCAGCCTGGGTGACAGAGGGGAGACTCTGTCTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKC 315
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                                                                                            (first entry)
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16163; , ,

Gaps

7933 135 0

7813 255 7873

20-OCT-2000 20-OCT-2000 20-OCT-2000 01-NOV-2000 08-NOV-2000 08-NOV-2000

17-NOV-2000;
10-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;

22-AUG-2000; 2000US-0227102P: 23-AUG-2000; 2000US-0227009P: 30-AUG-2000; 2000US-0228924P: 01-SEP-2000; 2000US-0229343P: 01-SEP-2000; 2000US-0229343P: 01-SEP-2000; 2000US-0229343P: 01-SEP-2000; 2000US-0229343P: 06-SEP-2000; 2000US-0229343P: 06-SEP-2000; 2000US-023043P: 06-SEP-2000; 2000US-023043P: 08-SEP-2000; 2000US-0231243P: 08-SEP-2000; 2000US-0231243P: 08-SEP-2000; 2000US-0231244P: 08-SEP-2000; 2000US-0231244P: 08-SEP-2000; 2000US-0231244P: 08-SEP-2000; 2000US-0231241P: 08-SEP-2000; 2000US-0231241P: 08-SEP-2000; 2000US-0231298P: 14-SEP-2000; 2000US-023299P: 14-SEP-2000; 2000US-02396P: 25-SEP-2000; 2000US-02396P: 25-SEP-2000; 2000US-02396P: 25-SEP-2000; 2000US-02399P:	atic; gene t apiens. 57182-A2. 2001; 20000 -2001; 20000 -2000; 20000 -20000 -2000; 20000 -2000; 20000 -2000; 2000 -2000; 2000 -2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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  WO200155320-A2
                                      Homo sapiens.
                                                                            cancer;
                                                                                              Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                     Human reproductive system related antigen DNA SEQ ID NO: 6505.
                                                                                                                                                                           21-NOV-2001
                                                                                                                                                                                                               AAL03817;
                                                                                                                                                                                                                                                    AAL03817 standard; DNA; 16163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 41973; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
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                                                                        gene therapy;
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                                                                                                                                                                                                                                                                                                                                                    GGAAAAAAAAAAAAAAAAAAAAAAAAAAA
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Pred. No. 1e-33;
0; Mismatches 71;
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30-JUN-2000;
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02-MAR-2000;
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19-MAY-2000;
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2000US-0225213P
2000US-0225266P
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2000US-0225267P
2000US-022575PP
2000US-022575PP
2000US-0225759P
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2000US-0226868P
2000US-0227182924P
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2000US-0218290P.
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2000US-0215135P.
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17-NOV-2000;
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08-NOV-2000
                                   (HUMA-) HUMAN GENOME SCI INC
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2000US-0251988P.
2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
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2000US-0246528P
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2000US-0246524P.
2000US-0246525P.
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Rosen CA,

Barash

SC,

Ruben

SM;

New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

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RESULT 6
ADA02750
ID ADA02
XX ADA0
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Best Local
                                                                                                              WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; gene; ds.
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                                                                                                                                                                       Morris
                                                                                                                                                                                                                                                                                26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA02750 standard; DNA; 96593 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16163 BP; 5062 A; 3448 C; 3239 G; 4414 T; 0 U; 0 Other;
                                                                                                                                                                                                                                (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     İsolated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8172 GGTTCACGCCTGTAATCCCAGCACTCTGGGAGGCCGAGGCGGGTGGATCACCTGATGTCA
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nilarity 73.9%;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this secretary and the complete sequence data for this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a call a polypeptide (especially an antibody) that specifically
                                                                                                                                                                                                                                                       04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1268; 245pp; English
                26-DEC-2001; 2001WO-US051291
                                                        30-JAN-2003.
                                                                                        WO2003008583-A2
                                                                                                                           Homo sapiens
                                                                                                                                                             human; ds; cytostatic; cancer; neoplasm; adeno
                                                                                                                                                                                                                     Human IRF2
                                                                                                                                                                                                                                                                                           ADB72488
                                                                                                                                                                                                                                                                                                                               ADB72488 standard; DNA; 96593
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                                                                                                                                                               adenocarcinoma; sarcoma; gene.
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                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                gene therapy; vaccine; carcinoma;
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Pred. No. 1.8e-33;
1; Mismatches 57;
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RESULT 8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotide sequence selected from any of the 660 sequences nucleotide sequences carcinoma, a polynucleotide of the invention has cytostatic in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-2001; 2001US-00798586.
23-0CT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morris
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                                                                                                                                        Cytostatic;
                                                                                                                                                                                                 01-JAN-2004
                                                                                                                                                                                                                                                         ADC85230 standard; DNA; 96593
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                                                                      WO2003045230-A2
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                                                                                                                           c; gene therapy; vaccine; cancer; carcinoma-associated
transmembrane; intracellular; ds.
                                                                                                                                                                     genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adenocarcinoma,
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75.0%;
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Pred. No. 1.8e-33;
                                                                                                                                                                                                                                                         ВP
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                                                                                                                                            gene;
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02-DEC-2002; 2002WO-US038582

05-JUN-2003.

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ADM74345
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Matches 216;
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22-DEC-2000; 2000US-00747377
02-MAR-2001; 2001US-00798586
                                                                                                                US2004072154-A1
                                                                                                                                                                              cytostatic.
                                                                                                                                                                                            carcinoma associated protein;
                                                                                                                                                                                                          Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
                                                                                                                                                                                                                                             Human carcinoma associated (CA) nucleic acid
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                                               30-NOV-2001; 2001US-00997722.
                                                                                 15-APR-2004.
                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                               01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant nucleic acid comprising a nucleotide sequence of any the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
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75.0%;
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Pred. No. 1.8
                                                                                                                                                                                            CAP;
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New carcinoma associated gene or protein, useful composition for diagnosing or treating carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to new recombinant nucleic acids. The invention
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(ENGE/)
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  GTGAGACKCCGTCTCAAAAACAACAACAAAAAAACAAAAAAAAACCATAAG 354
                                              CTTGAACCCAGGCGGCGGAGGTTGCAGTGAGCCGAGATCGCACCAGCTTGGGTGACAAGC
                                                                                                                                                           TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                             TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                      ATGCCTGTAATCCCCAGCACTTCGGGAGGCCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                      TGAGATCGCAG-----AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGA 306
                                                                                                                                                                                                                  TCAAGATCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96593 BP;
                                                                                                                                {	t TGGGCATGGTGGCGGGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCG-1839} {	t t}
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                        ۲,
                                                                                                                                                                                                                                                                                                                                                                                      Score 158.4; DB 12; Length 96593; Pred. No. 1.8e-33; 1; Mismatches 57; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22979 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27672 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for preparing e.g., leukemia
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RESULT 10 ACN44354/c

В

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Query Match
Best Local Similarity
Matches 217; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for neutralizing the effect of CAP; (vi) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                Sequence 31898 BP; 7315 A; 9118 C; 8770 G;
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   321 CAAAAACAACAACAAAAAACAAAAAAACCATAAGACATTGTCCATCTGCGGTTCCCAGA 379
                                                                                                                       TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                  ACGCCTATAATCCCAGCACTTTGGAAGGCCAAGGTGGGCGGATCACTTGAGGCCAGGAAT
                                  CGAGACCACGCCTTTGCACTCCAGCCTGGGCGA-----CAGAGCGAGACTCTGTCT
                                                                                                                                                                  TCGAGACCAGCCTGGCCAAAATGGTGAAACCCCCGTCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                       ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                  TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                    CCGGAGTGGTGGGGCGCCTGTAGTCCCAACTACTCGGGAGGCGGAGGTTGCAGTGAGC
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72.6%;
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Pred. No. 8.8e-33;
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                                                                                                                                                                                                                                                                                                                                                                  6695 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              DB 11;
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ACN37240
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      ACN37240;
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/note= "Variable nucleotide G,T"
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note= "Variable nucleotide A,G"
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/standard_name= "Single nucleotide
/note= "Variable nucleotide A,G"
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/note= "Variable nucleotide T,C"
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                      standard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide A,G"
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Morris

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periodontal disease; polymorphism;
single nucleotide polymorphism.
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/note= "Variable nucleotide T,C"
                                                                                /standard_name= "Single nucleotide
/note= "Variable nucleotide A,G"
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/note= "Variable nucleotide G,A"
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note= "Variable nucleotide T,C"
"Variable nucleotide
"Variable nucleotide C,G"
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/note= "V=-
        /note=
33071
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33056
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/standard
/note= "Va
15882
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/standard_r
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/note= "Variable nucleotide C,T"
24796
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31500
               /*tag= ae
/standard_name= "Single nucleotide polymorphism"
/note= "Variable nucleotide C,T"
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/standard_
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note= "Variable nucleotide deletion,CT"
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note= "Variable nucleotide G,A"
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17751
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"Variable nucleotide G,A"
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"Variable nucleotide G,T"
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"Variable nucleotide A,G"
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riable nucleotide C,T"
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e nucleotide A,G"
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RESULT 12
ABT10719/c
ID ABT107
XX
AC ABT107
XX
O4-DEC
XX
U5
BHuman
XX
KW Human;
KW cytost

04-DEC-2002

(first entry)

ABT10719;

ABT10719 standard; cDNA; 122748

ВÞ

Human; breast specific gene; breast cancer; differential expression; cytostatic; gene therapy; gene; ss.

Human breast cancer associated coding sequence SEQ ID NO:

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Best Local Sim:
Matches 200;
                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for examination of periodontal disease in which generic polymorphisms are detected in one or more of genes. The method is useful for examination, diagnosis and assessment periodontal disease or risk of periodontal disease and the risk of its progression to severe, aggressive and chronic periodontal disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                         Single nucleotide polymorphisms associated with examination and assessment of susceptibility to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUBI-)
(KAMO/)
                                                                                                                                                                                                                                                                                                     Sequence 34796 BP; 7631 A; 9152 C; 9368 G; 8645 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-2003;
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                                                                                                                                                                                                                                                                                                                              sequence represents a polymorphic gene of
                                                                                                                                                                                                  ATGCCTGTAATCCTGGCACTTTGGGAGGCCAAGGCGTGTGGATCATTTGCGGTCAGGAGT
AAAAACAAAACAAACAAACAAACAAAAAAAAACAAC
                                                                                                              TGGGCATGGTGGCACACCCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                      CARARACAACAACAAAAAAAAAAAAAAACCATAAGAC 356
                                                                TGAGATCGCAGAGTGAGCCGAAATCACAGAGTCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                              TTGAGACCAGCCTGGCCAACATGATGAAACCCCCGCCTCTATTAAAAATACAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 150; Opp; Japanese.
                                                                                               TGGGCATGGTGGCGAGTGCCTGTAGTCCCAGCTACTCAGGAGGCGGAGGTTGCAGTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suzuki A,
                                                                                                                                                                                                                                                     Conservative
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/note= "Variable nucleotide G,T"
33127
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/note= "Variable nucleotide A,C"
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RESULT 13
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25-APR-2001;
23-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing breast cancer in a patient comprises detecting the 1-
gene expression in cell or tissue samples, where a differential
expression is indicative of breast cancer.
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AAC79009;
                                AAC79009 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to methods of diagnosing breast cancer in ient, which comprise detecting the Level of expression in a tissue clent, which comprise detecting the commission of the shown in ABT09867-ble of two or more genes selected from those shown in ABT09867-ble of two or more genes selected from those shown in ABT09867-ble of two or more genes selected from the genes indicates breast inlicates breast increase.
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                                                                                                                                                                                                                                                                                                                             TTGAGACCAACCTGACCAACATGGTGAAAACCCCCACCTCTACTAAAAAATACAAAAATTAGC
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                                                                                                                    CAAAAAAAAGAAAGAAAGAAAAGAAAAGAAAA 114043
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; 2001US-0286090P.
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Pred. No. 2.9e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the isolation of genes AAC78997-C79045 encoding CC 49 human secreted proteins AAB44335-B444382. The genes can be used to CC generate fusion proteins by linking to the gene for the human CC immunoglobulin GFC portion (AAC78988) for increasing the stability of the fusion protein as compared to the human protein only. The genes and CC proteins are useful for preventing, ameliorating or treating medical CC conditions, e.g. by protein or gene therapy. The genes are isolated from CC a range of human tissues disclosed in the specification. The nucleic CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and CC ovarian cancer, and other cancers of the adrenal gland, bone, bone immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, (e) infections diseases such as myocardial ischaemias; (d) wound healing (e) infections diseases such as viral, bacterial, fungal and parasitic confections.
                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fourty nine nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
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14-JAN-2000; 2000US-0176063P
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nes 224; Conserv
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                                                                                                                                                                   CACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGC
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                                                              CAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCACA
                                                                                                                                                                                                                                                    ATATTTTGTTTAAATGGAATCATACCAGGCTGGGCACAGTGCTCACGCCTGTAATCCTAG
CAATATGATGAAACCCCGTCTCTA-AAAAAATACAAAATTAGCCGGGCGTGGTGTCAGG
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 9.2e-33;
1; Mismatches 7(
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 884;
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Matches 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                           from patients suffering from this disease contain autoantibodies against a 30 kDa cochlear protein antigen. The disease is believed to be an autoimmune disease. The beta-twhulin antigen is useful as a target substance in diagnosing or detecting Meniere's disease and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a beta-tubulin antigen. The protein is an antigen of the membranous structure of the inner ear protein, and is reactive with antibodies from patients having Meniere's disease. Serum Meniere's disease a chronic ear disease with unknown etiology. Serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New beta-tubulin antigen in the membranous structure of the inner ear, reactive with antibodies of patients with Meniere's disease, for diagnosing Meniere's disease and distinguishing this disease from othe
                                                                                                                                                                                                                                                                                                                                                                 Sequence 14784 BP; 5454 A; 2966 C;
                                                                                                                                                                                                                                                                                                                                                                                                                              distinguishing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing Mėniere's disease autoimmune ear diseases.
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TCCCAGCACTTTGGGAGGCCAACGTGGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAG
                                                         TCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCAT 150
                                                                                                                     GATCTAAGAATTTATTATAAAAGTGTAGCAAGGGCTGGGCGCGGGGCGCCTCACGCCTGTAA
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                                                                                                                                                                                                                                        Score 153.2; DB 3;
Pred. No. 2.9e-32;
D; Mismatches 128;
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       for use in evaluating the prognosis of patents suffering from acute myelogenous leukemia (AML) by analysis of the patients gene expression profile. The invention relates to a novel method for evaluating the prognosis of a patient with acute myelogenous leukemia by detecting higher/lower expression level of genes encoding mRNA recognized by a probe set chosen from 19 nucleotide sequences (AEE03340 or AEE03344-AEE03361). Also, gene expression profiling of AML patients using a set of probes based on 167 sequences (AEE03362-AEE03527) using a biochip was performed to determine prognosis. Methods are also included for determining an AML patient's state, determining AML patient's treatment protocol, determining whether the patient will respond to the treatment, and producing an AML patient's prognosis report by analysis of the patients gene expression profile. The methods are useful in evaluating an AML patient's prognosis and for treating AML patient.
                                                                                                                                                                                                                                                                                                                                      Evaluating an acute myelogenous leukemia patient's prognosis, comprisin detecting lower or higher expression level of gene recognized by probe set e.g. 202820-at and 206148-at, with respect to predetermined cut-off
                                                                                                                                                                                                                                                                                         Example
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                                                                                                                                                                                                                                                     The present sequence is that of a human gene sequence which is claimed
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PR 04-FEB-2000; 2000US-0180525F. PR 04-FEB-2000; 2000US-018050F. PR 16-MAR-2000; 2000US-018050P. PR 16-MAR-2000; 2000US-018050P. PR 16-MAR-2000; 2000US-0199123P. PR 17-MAR-2000; 2000US-0199123P. PR 19-MAY-2000; 2000US-0209467P. PR 28-JUN-2000; 2000US-020467P. PR 28-JUN-2000; 2000US-021635P. PR 07-JUL-2000; 2000US-021647P. PR 07-JUL-2000; 2000US-021680P. PR 11-JUL-2000; 2000US-0217487P. PR 11-JUL-2000; 2000US-0217496P. PR 11-JUL-2000; 2000US-0217496P. PR 11-JUL-2000; 2000US-0217496P. PR 11-JUL-2000; 2000US-0218390P. PR 14-JUL-2000; 2000US-0220964P. PR 14-JUG-2000; 2000US-022964P. PR 14-JUG-2000; 2000US-022964P. PR 14-JUG-2000; 2000US-0229513P. PR 14-JUG-2000; 2000US-0225214P. PR 14-JUG-2000; 2000US-0225216P. PR 14-JUG-2000; 2000US-0225266P. PR 14-JUG-2000; 2000US-0225266P. PR 14-JUG-2000; 2000US-0225266P. PR 14-JUG-2000; 2000US-0225266P.	SULT 16 L04959/c AAL04959; AAL04959; 21-NOV-2001 Human reprod Human; reprod cancer; gene Homo sapiens WO200155320- 02-AUG-2001. 17-JAN-2000:	Sequence 166942 BP; 42646 A; 40900 C; 40852 G; 42544 T; 0 U; 0 Other; Duery Match 38.2%; Score 152.8; DB 15; Length 166942; Best Local Similarity 75.0%; Pred. No. 7.8e-32; Matches 219; Conservative 1; Mismatches 63; Indels 9; Gaps 2; Matches 219; Conservative 1; Mismatches 63; Indels 9; Gaps 2; Db 33655 CCTATAATCCCAGCACTTTGGGAGGCCAAGGTGAGATCACCTGAAGATCACGAGATCCG 3371 Qy 144 AGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAATTAGCTGG 203 Db 33715 AGACCAGCCTGGCCAACATGGTGAAATCCCATCTTACTAAAAATACACAAAAATTAGCTGG 3377 Qy 204 GCATGGTGGCAACATGGTGAAATCCCAGCTACTTCAGGAGCTGAGATTGCAGTGAGCTGA 263
02-0CT-2000; 2000US-023 13-0CT-2000; 2000US-023 13-0CT-2000; 2000US-023 13-0CT-2000; 2000US-023 20-0CT-2000; 2000US-024 20-0CT-2000; 2000US-024 08-NOV-2000; 2000US-024	PR 14-SEP-2000; 2000US-023; PR 21-SEP-2000; 2000US-023; PR	PR 14-AUG-2000; 2000US-0225447P. PR 14-AUG-2000; 2000US-0225447P. PR 14-AUG-2000; 2000US-0225757P. PR 14-AUG-2000; 2000US-0225758P. PR 14-AUG-2000; 2000US-0225759P. PR 18-AUG-2000; 2000US-02266681P. PR 22-AUG-2000; 2000US-0226668P. PR 22-AUG-2000; 2000US-0226688P. PR 22-AUG-2000; 2000US-0227182P. PR 22-AUG-2000; 2000US-0227182P. PR 23-AUG-2000; 2000US-0229344P. PR 01-SEP-2000; 2000US-0229344P. PR 01-SEP-2000; 2000US-0229345P. PR 01-SEP-2000; 2000US-0229345P. PR 01-SEP-2000; 2000US-0229345P. PR 01-SEP-2000; 2000US-023945P. PR 05-SEP-2000; 2000US-023945P. PR 06-SEP-2000; 2000US-023943P. PR 06-SEP-2000; 2000US-023144P. PR 08-SEP-2000; 2000US-0231244P. PR 08-SEP-2000; 2000US-023144P. PR 08-SEP-2000; 2000US-0231414P. PR 08-SEP-2000; 2000US-023144P. PR 08-SEP-2000; 2000US-0

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                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention
                                                                                                                              y Ma
c Local 5.
                                                                                                                                                                                      Sequence 4388 BP;
                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a reproductive system ant used in preventing, treating or ameliorating a medical condition.
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                                                          TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                   TGGGCATGGTGGCACACCCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTTGCAGTGAGC
                                           TCGAGACCAGCCTGGCCAACATGGTGAAACTCCGTCTCTACTAAAAATTACAAAAATTAGC
                                                                                          AAGCCTGTAATTCCAGCACTTTGGGAGGCCGAGGCCGGATCACTTGAGGTCAGGAGT
CĠCAĊĠTĠĠTĠĠĊĠĊĠĊĠĊĊŦĠŦĀAŦĊĊĊĀĠĊŦĀĊŦĊĠĠĠĀĠĠĊĠĠĀĠĠŦŦĠĊĀĠĊĠĀĠĊ
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                                                                                                                                                                                                                                                                              SEQ ID NO 7647; 1297pp + Sequence Listing;
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2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
2000US-0251868P.
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2000US-0246631P.
2000US-0246611P.
2000US-0246611P.
2000US-024920P.
2000US-024920P.
2000US-0249210P.
2000US-0249211P.
2000US-024921P.
2000US-024929P.
2000US-024929P.
2000US-024929P.
2000US-025039P.
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                  SC,
                                                                                                                                                                                   870 A; 1238 C; 1205 G; 1075 T; 0 U; 0 Other;
                                                                                                                                                  38.1%;
                                                                                                                                                                                                                                                                                                                                                                                          SCI
                                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                                                                                       Score 152.4; DB 4;
Pred. No. 3.3e-32;
1; Mismatches 52;
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                                                                                                                                                            Length
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                                                                                                                                                             4388;
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RESULT 17
ABL97853/c
ID ABL97853;
XX
ABL97853;
XX
ABL97853;
XX
ABL97853;
XX
AC ABL97853;
XX
DT 21-JUN-200
XX
Human; test
XX
Hu
   11-JUL-2000
11-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
14-AUG
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28-JUN-2000;
30-JUN-2000;
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17-MAR-2000;
18-APR-2000;
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07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001;
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2000US-0225759P
2000US-022681P
2000US-022688P
2000US-022688P
2000US-02271082P
2000US-0227099
2000US-0228924P
2000US-02289287P
2000US-0229343P
2000US-0229345P
2000US-0229345P
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2000US-0190076P.
2000US-019123P.
2000US-0205515P.
2000US-0214886P.
2000US-0214886P.
2000US-0215135P.
2000US-0216880P.
2000US-0217487P.
2000US-0217487P.
2000US-0218290P.
2000US-022964P.
2000US-0224518P.
2000US-0224518P.
2000US-0225213P.
2000US-0225213P.
2000US-0225266P.
2000US-0225264P.
2000US-02252479P.
2000US-02252479P.
2000US-0225247P.
2000US-0225247P.
2000US-022575P.
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2000US-0186350P
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Best Local S
Matches 202
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic
                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                      fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids encoding
                                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGACAGAGTGAGACKCCGTCT
                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC
                CAAAAACAACAACAAAAAACAAAA
                                                                                                             CGCACGTGGTGGCGCGCCTGTAATCCCAGCTACTCGGGAGGCGGAGGTTGCAGCGAGC
                                                                                                                              TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                    TCGAGACCAGCCTGGCCAACATGGTGAAACTCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                              ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                                                            4388 BP;
                                                                                                                                                                                                                            AAGCCTGTAATTCCAGCACTTTGGGAGGCCGAGGCCGGATCACTTGAGGTCAGGAGT
CAAAAAAAAAAAAAAAAAAA
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2000US-0249217P.
2000US-0249218P.
2000US-0249244P.
2000US-0249265P.
2000US-0249269P.
2000US-0249299P.
2000US-0249299P.
2000US-0251030P.
2000US-0251130P.
2000US-02511988P.
2000US-02511856P.
2000US-0251868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2505; 766pp; English
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing
                                                                                                                                                                                                                                                                                                                                          870 A; 1238 C; 1205 G; 1075 T;
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                                                                                                                                                                                                                                                                                                 38.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human testicular antigen polypeptides, and/or treating testicular cancer.
                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MS
                                                                                                                                                                                                                                                                                     Score 152.4; DB 4;
Pred. No. 3.3e-32;
1; Mismatches 52;
 1021
                            344
                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                             0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                    4388;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
11-SEP-2000;
11-SEP-2000;
11-SEP-2000;
11-SEP-2000;
11-SEP-2000;
11-SEP-2000;
11-SEP-2000;
12-SEP-2000;
13-OCT-2000;
13-OC

2000US-0229509P.
2000US-0239509P.
2000US-023043PP.
2000US-0231443P.
2000US-0231244P.
2000US-0231244P.
2000US-02312413P.
2000US-0231413P.
2000US-0231413P.
2000US-0231413P.
2000US-0231414P.
2000US-023142P.
2000US-024611P.
2000US-0

RESULT 18 ABL68122/c ID ABL68122 s

ABL68122/C ID ABL68122 standard; DNA; 174424 BP.

15-MAY-2002 ABL68122;

(first entry)

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28-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
02-OCT-2000
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25-SEP-2000
25-SEP-2000
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25-SEP-2000
26-SEP-2000
26-SEP-2000
Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                              28-SEP-2000;
28-SEP-2000;
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22-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                    (AVAL-) AVALON PHARM.
                                       2002-188264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer related gene sequence SEQ ID NO:6459
                                                         Augustus M,
Weaver Z;
                                                                                                   2000US-023563BP
2000US-023571LP
2000US-023572DP
2000US-0235863P
2000US-0236033P
2000US-0236033P
2000US-0236112P
2000US-023612P
2000US-023612P
2000US-0237172P
2000US-0237172P
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2000US-0237172P
2000US-023729BP
2000US-023729BP
2000US-023729BP
2000US-023729BP
2000US-0237425P
2000US-023760BP
2000US-023760BP
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2000US-0209531P.
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CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC prostate, near convolution of the cancer such
CC prostate or pancreatic cancer adenocarcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                           48262
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                                                                                                                                                                                                                                                                          CATGGCA----GCTCATGCCTGTAATCCCAACACTTTGGGAGGCCGAAGTGGGCGGATCA
GAGGCAGGAGAATCGCTTGAATCCGGGAGGTGGAGATTGCAGTGAGCCGAGATTGTGC
                                           GAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                                                                    AATACAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 6459; 44pp; English
                                                                                                                                                                                 CCTGAGGTCAAGAGATCAAGTCCATCCTGGCCAACATGGTGAAACCCCTGTTTGTACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 152; DB Pred. No. 1.3e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 174424; .3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
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ARESULT 19
ADQ19573/c
ID ADQ195
XX ADQ195
XX ADQ195
XX ADQ195
XX Boft t
XX Boft t
XX Boft t
XX Homo s
XX H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
ds.
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                                                                                                                                                                                       26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                             26-NOV-2003; 2003WO-US038193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human soft tissue sarcoma-upregulated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ19573 standard; DNA; 181343 BP
                                                          (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LO-JUN-2004.
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RESULT 20
ABQ88186/c
ABQ88186;
XX
AC: ABQ88186;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human osteoblast differentiation rela
XX
CS Human; osteoblast; stem cell differen
XX
XX
CS Human;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
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                                                                                                                                                                                                                                                                                                                                     Human; osteoblast; stem cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 181343 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TACTCAGCCATGTGCTGGGCCATGGGAACCCCAAATATTAATAAGACATTGTCAGGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGCAGGAGATCGCTTGAATCCGGGAGGTGGAGATTGCAGTGAGCCGAGATTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGAGGTCAAGAGATCAAGTCCATCCTGGCCAACATGGTGAAACCCCTGTTTGTACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCAGGTGTCTGGTGATCCTTGGTTGTCTTCTCATATTTAAGAATGGGGCAGGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATACAAAAATTAGCTGGGCATGGTGGTACGCACCTGTAGTCCCAGCTACTTGGGAGCCT 48204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATGGCA----GCTCATGCCTGTAATCCCAACACTTTGGGAGGCCGAAGTGGGCGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2392;
                                                                                                                                                                                                                                                                                                                                                                                                     differentiation related cDNA SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 152; DB 12;
Pred. No. 1.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                            bone tissue deposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 181343;
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                                                                                                                                                                                                                                                                                                                                                                                                            NO
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RESULT 21
AAK68418/c
ID AAK684
XX
AC AAK684
XX
DT 06-NOV

standard; DNA; 14282

ВP

06-NOV-2001 AAK68418; AAK68418

(first entry)

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis; or (c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition. Specific conditions include postmenopausal osteoporosis glucocorticoid osteoporosis or male osteoporosis, osteopenia, osteodystrophy, druginduced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to genes and their expression profiles are used for: (a) screening modulators of precursor stem cell differentiation osteoblasts, or bone tissue deposition; (b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-557663/59
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24-APR-2001; 2001US-0285691P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 169739 BP; 49809 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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125593
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                                   325
                                                                                                              270
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PROCTER & G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                ggaacccaaatattaataagacattgtcaggccaggcatgacactggctgaatgcctgta
                                                                                                                                                                                                                                                                                                                                                                                 GGTAAGAAAATCTTAGTTAAAGATCTAAAGTTTGGCCAGGCACAGTGGCTAACGCCTGTA 125833
                                                                                                                                                                                                                                                    TCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGG 209
                                                                                                                                                                                                                                                                                                      ATCCCAGCACTTCGGGAGGCCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTCGAGACCA 125773
                                                                       TGGGTGAGTCAAGATCGCAACATGGCACTCCAGCCTGGGCAACAGAGACTCCATCTCCAA 12559
                                                                                                                                                                         TGGCACACACCTGTAGTCCCAGCTACTCAGGAGGCCGGAGATTGCAGTGAGCTGAGATCGC 269
                                                                                                                                                                                                                             GCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGG
                                                                                                                                                                                                                                                                                                                               ATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCA 149
                                                                                                              AGAGTGAGCCGAAATCACA----GATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA 324
AAAAATAAATAAATAAAAATAA 125571
                                   ААСААСААСААААААСАААААА 347
                                                                                                                                                    TGGCAGACACCTGTAGTCCCAACTACTCAAGAGGCTGAGGCAGGAGAATCACTTGAAC-C
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70.9%;
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Pred. No. 1.9e-31;
1; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U; 0 Other;
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MAR - 2000 JUN - 2000 JUN - 2000 JUN - 2000 JUN - 2000 JUL - 2000	Human immune/h Human; immune; Cytostatic; ge Homo sapiens. WO200157182-A2 09-AUG-2001. 17-JAN-2000; 2 04-FEB-2000; 2 02-MAR-2000; 2 16-MAR-2000; 2
2000US-0199076P 2000US-019913P 2000US-0205515P 2000US-0215135P 2000US-0215647P 2000US-02174886P 2000US-0217488P 2000US-0217488P 2000US-0217496P 2000US-0217496P 2000US-0217496P 2000US-0225964P 2000US-0225213P 2000US-0225266P 2000US-0225266P 2000US-0225267P 2000US-0225275P 2000US-022575P 2000US-022570B 2000US-022570B 2000US-022570B 2000US-022570B 2000US-022570B 2000US-022570B 2000US-022570B 200U	ne therapy; vacci ne therapy; vacci ne therapy; vacci 001WO-US001354. 000US-0180528P. 000US-0180528P. 000US-0180550P.
	igen genomic sequence SEQ ID NO:23230. immune/haematopoietic antigen; cancer; ine; metastasis; ds.
	<u>.,</u> .,
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13-CCT-2000; 20-CCT-2000; 20-NOV-2000; 20-CCT-2000; 20-NOV-2000; 20-CCT-2000; 20-CC	14-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 20-SEP
2000US-0249214P 2000US-0241960P 2000US-0241785P 2000US-0241785P 2000US-0241809P 2000US-0244617P 2000US-0244617P 2000US-0244617P 2000US-0246475P 2000US-0246478P 2000US-0246478P 2000US-0246478P 2000US-0246524P 2000US-0246524P 2000US-0246528P 2000US-0246528P 2000US-024652P 2000US-024652P 2000US-024652P 2000US-024652P 2000US-024652P 2000US-024652P 2000US-024651P 2000US-024651P 2000US-024651P 2000US-024951P 2000US-024921P	2000US-023306; 2000US-023427; 2000US-023499; 2000US-0235489; 2000US-023548; 2000US-023548; 2000US-02363; 2000US-02363; 2000US-02363; 2000US-023636; 2000US-023636; 2000US-023637; 2000US-02373; 2000US-02373; 2000US-02373; 2000US-02373; 2000US-02373; 2000US-02373; 2000US-02373; 2000US-02373;

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RESULT 22
AAS28363/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynuclectides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (II, by inserting the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK64703 and AAM62169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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08-DEC-2000; 2000US-0251990P.
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05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 23230; 3071pp + Sequence Listing; English
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Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
                                                Genomic sequence #203 encoding for novel human respiratory antigen.
                                                                                  07-NOV-2001
                                                                                                                  AAS28363;
                                                                                                                                               AAS28363 standard; DNA; 32146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14282 BP; 3993 A; 2449 C; 2814 G; 5026 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATAATGTTATCCTGGCCAGGCACGGGGCACATGCCTGTAATCCCAGCACTTTGGGAG
                                                                                                                                                                                                                                  GGGCAACAGAGTGAACTCTGT 4524
                                                                                                                                                                                                                                                                                               GCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGA 167
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                                                                                                                                                                                                                                                    AGATCACAGAGTGAGCAGAGT 308
                                                                                                                                                                                                                                                                                                                                                                                             AACCCCGTCTTTACTAAAAATACAAAAATAGCTGGGCATGGTGGCACACCTGTAGTC
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73.6%;
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Pred. No. 1.5e-31;
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respiratory active; ds.
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RESULT 23
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Matches 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of novel human respiratory antigens (AAUI7685-AAUI7975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, consilittis, and laryngitis), lung disorders (e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treating, preventing and/ or disorders related to the respiratory system including and also for testing and detection e.g. diagnosis.
 respiratory system antigen; human respiratory system associated polynucleotide;
                                 antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
                                                                  Human respiratory system associated
                                                                                                                                                                         ADG41559
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Pred. No. 1.9e-31;
1; Mismatches 95
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respiratory system disorder; who at disorder; vecal cord paralysis; chesilitis; largingtis; lung disorder; vecal cord paralysis; chesilitis; largingtis; lung disorder; cystic fibrosis; empty cambon, a alteryic disorder; latingtory cystic fibrosis; empty cember; latingtory cystic fibrosis; empty cember; latingtory cystic fibrosis; empty emman, a latingtory common and latingtory cystic fibrosis; empty emman, a latingtory cystic fibrosis; empty emman, a latingtory cystic fibrosis; empty emman, and cambon of the nose; gahe theory cystic fibrosis; latingtory emman, and cambon of the nose; gahe theory cystic fibrosis; latingtory empty emman, and cambon of the nose; gahe theory cystic fibrosis; latingtory empty emman, and cambon of the nose; gahe theory cystic fibrosis; latingtory empty emman, and cambon of the nose; gahe theory cystic fibrosis; latingtory empty emman, and cambon of the nose; gahe theory cystic fibrosis; latingtory empty emp	
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14-SEP-21-SEP-221-SEP-221-SEP-221-SEP-221-SEP-225-SEP-225-SEP-225-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-227-SEP-	
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2000US-0251868P

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The invention describes an isolated polypeptide (I) comprising an amino acid sequence that is at least 90% identical to polypeptide fragment of the polypeptide fragment of the polypeptide fragment of the polypeptide described fragment of the polypeptide described fragment of the polypeptide described fragment of the protein of ps, or variant, allelic variant or species homolog of ps. (I) or a polypucleotide (II) encoding (I) is also useful for diagnosing a polypucleotide fragment or susceptibility to a pathological condition or a susceptibility to a pathological condition in a subject which involves determining the presence or absence of mutation in a subject which involves determining the presence or absence of mutation of in (II) or determining the presence or absence of mutation of in (II) or determining the presence or absence of mutation of in (II) or determining the presence or absence of mutation of in (II) or determining the presence or absence of mutation of the polypeptides are useful in diagnosis, at the treatment, prevention and/or (II) in a condition based on the prognosis of disorders of respiratory system such as throat disorders (e.g., pneumonia), pleurisy, cystic fibrosis, emphysema, histiocytosis, and largic disorders (e.g., asthma and eosinophilic pneumonia), pleurisy, cystic fibrosis, emphysema, histiocytosis, and concers of the nose). The polynucleotides are useful in gene therapy techniques, for chromosome identification, identifying individuals from
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Best Local S
Matches 224
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08-DEC-2000; 2000US-0251999P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
17-JAN-2001; 2001US-00764860.
14-FEB-2002; 2002US-00074095.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                            KCCGTCTCAAAAACAACAACAAAAAACAAAAAACCATAAGACATTGTCCATCTGCGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                          TCTCAGCAAATACTGGATTTAACAAAG 2111
                                                                                                                                                                       CCCAGACTATTGCAGGAGACCAAAAAG 400
                                                                                                                                                                                                                                                                 AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGCATGGTGGCGGGCACCTGTAGTCCCAGCTGCTTGGGAGACTGAGCCAGGAGAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGAGACAAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGCCTGTAATGCTAGCACTTTGGGAGGCCAAGGCGGAGGATCACTTGAGGTCAGGAGT
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RESULT 24
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XX AD197333/c
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XX AD197
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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

26-JUL-2000;

17-MAR-2000;

2000US-0184664P. 2000US-0186350P. 2000US-0179065P 2000US-0180628P.

14-FEB-2002;

2002US-00074095

14-AUG-2000; 14-AUG-2000;

14-AUG-2000;

2000US-0189874P.
2000US-0198123P.
2000US-0198123P.
2000US-0205515P.
2000US-0215135P.
2000US-0216880P.
2000US-0216880P.
2000US-0218890P.
2000US-0218890P.
2000US-0224518P.
2000US-0224518P.
2000US-0224518P.
2000US-0225213P.
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14-AUG-2000; 18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 23-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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respiratory system-related polypeptide; antiasthmatic; antibacterial; antiinflammatory; cytostatic; antianaemic; antiallergic; gene therapy; pneumonia; lung cancer; cystic fibrosis; asthma; sarcoidosis; rhinitis; anaemia; leukaemia; inflammation; sinusitis;
Homo sapiens
                                                                        chronic obstructive pulmonary disease; infectious disease; human; ds
                                                                                                                                                                                                                                                                                             Human respiratory system associated polypeptide-related DNA SeqID797.
                                                                                                                                                                                                                                                                                                                                                                      04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI97333;
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08-SEP-2000; 08-SEP-2000; 12-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0232080P.
2000US-0232081P.
2000US-0231968P.
2000US-0232397P.
2000US-0232398P.
2000US-0232398P.
2000US-0232398P.

14-SEP-2000; 14-SEP-2000;

2000US-0233065P. 2000US-0234223P. 2000US-0234274P. 2000US-0234997P. 2000US-0234998P.

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Matches 224
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention is related to a novel isolated polypeptide, which comprises a human respiratory system-related polypeptide, and the DNA sequence which encodes it. The invention may be useful for the development of compounds with an antiasthmatic, antibacterial, antiinflammatory, cytostatic, antianaemic or antiallergic activity. In addition, the sequences disclosed may be useful for gene therapy. The polypeptide or polynucleotide is useful for treating, preventing or ameliorating a medical condition, for example pneumonia, lung cancer, cystic fibrosis, asthma, sarcoidosis, rhinitis, anaemia, leukaemia, inflammations, sinusitis, chronic obstructive pulmonary disease or infectious diseases. The polypeptide or polynucleotide is also useful for diagnosing any of these diseases or a susceptibility to the disease. The present sequence is that of a human DNA sequence which is related to a business of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human treating, fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAG-----
                                                                                                                                                                                                                                                                                                                                                               TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32146 BP;
  TCTCAGCAAATACTGGATTTAACAAAG
                                                                      TCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGATAAAAGTAGAGACAATAGGGGGA
                                                                                                                                                                                                          AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGAC
                                                                                                                                                                                                                                                                                                                                       TTGAGACAAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCCTGTAATGCTAGCACTTTGGGAGGCCAAGGCGGGGGATCACTTGAGGTCAGGAGT
                                       CCCAGACTATTGCAGGAGACCAAAAAG 400
                                                                                                                        KCCGTCTCAAAAACAACAACAAAAAAAACAAAAAAACCATAAGACATTGTCCATCTGCGGTT
                                                                                                                                                                  CTTGAACCCGGGAGGCTGCAATGAGCCGAGATTGTACTACTGCAATGCAGAGAC
                                                                                                                                                                                                                                                     AGGGCATGGTGGCGGGCACCTGTAGTCCCAGCTGCTTGGGAGACTGAGCCAGGAGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 respiratory system-related polypeptide and genes, useful for preventing or diagnosing e.g. pneumonia, lung cancer, cystic asthma, sarcoidosis, rhinitis, leukemia, inflammations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
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2000US-0250391P.
2000US-0251030P.
2000US-0251988P.
2000US-0251479P.
2000US-0251866P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-025499PP.
2000US-025499PP.
2001US-025499PP.
2001US-0259678P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system associated gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8745 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 150.6; DB 11;
Pred. No. 1.9e-31;
1; Mismatches 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention.
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2000US-0241869P.
2000US-0241869P.
2000US-0246476P.
2000US-0246476P.
2000US-0246477P.

14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
27-CCT-2000;
27-CC

S-0246478P. S-0246523P. S-0246524P. S-0246525P.

2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246610P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0249611P 2000US-024920P 2000US-024921P 2000US-024924P 2000US-024929P 2000US-024929P

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RESULT 25
ADL13941/c
ID ADL139
XX ADL139
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Best Local Similarity
Matches 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             individual to joint space narrowing and/or osteophyte development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polynucleotide encoding at least one of the protein listed in the specification. The methods, composition and agent are useful for modulating the susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarthritis. The cell line and the non-human animal are useful for screening for an agent for diagnosing an individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint pain. This sequence corresponds to the polynucleotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification by was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polymucleotide encodition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 125515 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a procein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2001; 2001US-0342603P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoarthritis; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; gene; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoarthritis-associated polymorphic nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
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                                                                                                                                                                                                                                                          ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCCGATCACCTGAGGTCAAGAGA 140
                                                                                                                         TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                 ATGCTTGTAATCCCAGCACTTTGGGAGGCTGAGGAGGGCGGATTATTTGAGGTCAGGAGT
             TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schafer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                               Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  narrowing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IJ
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osteophyte development; joint pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297pp; English.
                                                                                                                                                                                                                                                                                                                                        Score 150.6; DB Pred. No. 3e-31; Mismatches
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21-JUL-1998;
22-DEC-1998;
                                                   degeneration caused by injury or diseases of nerves within the CNS or PNS. Such injury includes spinal cord injury, blunt trauma, penetrating trauma, haemorrhagic stroke or ischaemic stroke, whilst diseases include diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
                                                                                                         The present sequence is a gene encoding human myelin oligodendrocyte glycoprotein which is a nervous system-specific antigen. The antigen or peptides derived from it activate T cells in vivo. The present sequence is used to promote nerve regeneration or to prevent or inhibit neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; myelin oligodendrocyte glycoprotein; MOG; NS-specific antigen; nervous system-specific antigen; T cell; peripheral nervous system; ENS; nerve regeneration; neuronal degeneration
                                                                                                                                                                                   Claim
                                                                                                                                                                                                          New compositions useful to treat nervous system traumatic injury, Alzheimer's disease etc.
                                                                                                                                                                                                                                                                                               Eisenbach-Schwartz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spinal cord injury; blunt trauma; penetrating trauma; senile dementia; ischaemic stroke; diabetic neuropathy; glaucoma; haemorrhagic stroke; Alzheimer's disease; Parkinson's disease; Huntington's chorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human myelin oligodendrocyte glycoprotein gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amyotrophic lateral sclerosis; ALS; treatment;
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MCINNIS P A.
                                      glaucoma,
                                                                                                                                                                                Fig 18;
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98WO-US014715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "myelin oligodendrocyte glycoprotein"
/note= "Reading frame is interrupted by introns
precise location of which is not given in the
                                                                                                                                                                              92pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                      Huntington's chorea, amyotrophic
                                                                                                                                                                                 English.
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                                                                                                                                                                                                                                                                                                Mosonego
                                                                                                                                                                                                                           injury
                                         lateral sclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degeneration;
                                                                                                                                                                                                                            disease
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Sequence 17538

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XW Centr
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XW Nootc
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1998;
22-DEC-1998;
19-MAY-1999;
The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering
                                                                                                                                                                                            Promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, comprises administering nervous system-specific activated T cells/antigen, or
                                                                                                                                                                                                                                                                                                                                                                                                                          Eisenbach-Schwartz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUN-2001; 2001US-00893348.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic; osteopathic; vasotropic; nephrotropic; cytostatic; antiqen: dene the myelin oligodendrocyte olyopropic; cytostatic; antiqen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS; central nervous system; tranquillizer; MOG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human myelin oligodendrocyte glycoprotein (MOG) gene sequence.
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                                                                                                                                                                  analogs/peptides.
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DB; ABB81071.
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                                                                                                             Fig 18; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98IL-00124500.
98WO-US014715.
98US-00218277.
99US-00314161.
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72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                          Hauben
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Pred. No. 1.8e-31;
0; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽₽
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                                                                                                                                                                                                                                                                                                                                                                                                                          Beserman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 28 ADQ97695/c

ADQ97695

standard; DNA; 88892

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Cytostatic;

Gene

Therapy; cancer; leukemia; lymphoma; Human; ds

22-DEC-2003; 2003WO-US041389

WO2004060304-A2

07-OCT-2004

(first entry)

Human cancer associated sequence HD10-029, SEQ ID

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC damages caused by surgery such as tumour excision. The disease is not an CC autoimmune disease or neoplasm. The disease results in a degenerative CC process occurring in either gray or white matter or both. The disease is CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and CC experimental selections, intervertebral dise herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral CC neuropathies associated with various diseases, including but not limited CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute CC esnsory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary cC amyloidosis, obstructive lung diseases, acromegaly, malabsorption CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-CC pathies, complications of various drugs (e.g., metronidazole) and toxins CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangectasia, Friedreich's ataxia, amyloid polyneuropathies, Fabry's CC disease, or lipoproteinemia. The present sequence represents a human of control of the present sequence represents a human of control of the present sequence represents a human of the control of the present sequence and a meannile of NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17538 BP; 4624 A; 4120 C; 3991 G; 4803 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myelin oligodendrocyte glycoprotein (MOG)
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                                                                                                                                                                                                                   TGGGCATGGTGGCACACACCTGTAGTCCCAGCTTACTCAGGAGCCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                  TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
AAAAAACTTCATCTCAAAAAAAAAAGAAAGAAA
                                            CAAAAACAACAAAAAAAACAAAAAAACCATA
                                                                                            CTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCATCTCA 13289
                                                                                                                                      TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                        TGGGCATGGTGGCATGCGCCTGTAGTTCCAGCAACTTGGGAGGCTGAGGCAGGAGAATCG 13349
                                                                                                                                                                                                                                                                                      TCAAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.6%;
72.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 150.4;
Pred. No. 1.8
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8e-31;
                                               352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene sequence, an example of NS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17538;
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RESULT 29
AAI61042
ID AAI61
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Best Local S
Matches 204
                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance; peripheral nervous system; CNS; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; huntington's disease; hamemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI61042 standard; cDNA; 4779
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                                                             26-JUL-2001.
                                                                                                                     WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 5031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morris DW,
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                                                                                                                                                                                                                                                leukaemia; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Pred. No. 3e-
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26-DEC-2000; 2000WO-US034263

RESULT 30 AED18472

AED18472

standard;

DNA;

100998

BXGXAXU

15-DEC-2005

(first entry)

Fibrotic disorder associated polynucleotide SEQ ID

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                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                                                                                                                                                                                                                                                                      immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheiner's, Parkinson's disease, Huntington's disease, such as Alzheiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
Wang
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful as central nervous system injuries.
                                                                                                                                                                                                                                                                                               Sequence 4779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 5031; 10078pp; English.
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03-AUG-2000;
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20-JUN-2000;
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21-JAN-2000;
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19-OCT-2000;
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Wang Z,
Goodrich
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                                                                               TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
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CGAGATTGCGCCACTGCACTCCAGCCTGGGCGACACAGTGAG
                          TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG
                                                        TGGGCGTGGTGGCACATGCCTGTAGTCCCAGCTATTTGGGAGGCTGAGGCTGCAGTGAGC
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2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
2000US-00620315.
2000US-0062191.
2000US-00693036.
2000US-00693036.
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Wehrman T,
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Xu C,
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Zhang J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; gene therapy;
therapeutic; diagnosis; uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide encoded by the differentially-expressed gene, in a cell population for preparing a composition for diagnosing or treating fibrotic disorders, e.g. uterine fibrosis. This sequence represents a polynucleotide associated with detection and treatment of fibrotic disorders. Note: This sequence does not appear in the printed specification but has been obtained in electronic format directy from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a modulator of a gene that is differentially-expressed in fibrotic tissue or during fibrogenesis, or a polypeptide encoded by the gene, in a cell population by contacting the cell population with a test
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19-OCT-2004; 2004US-0620444P.
15-DEC-2004; 2004US-0636240P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100998 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 723; 202pp; English
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93164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                       GCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAGTACAAAAATCAGCCAGGCATGG
TGGCAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGAATCACTTGAACCCTGGAGGC
                                                        TGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGC
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Pred. No. 4.1e-31;
1; Mismatches 81
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fibroids; gynecological; inflammation;
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<pre>/*tag= an /standard_name= "Single nucleotide polymorphism" 92791</pre>	86161 /*tag= am /standard_name= "Single nucleotide polymorphism" 92229	<pre>/*tag= al /standard_name= "Single nucleotide polymorphism"</pre>	/*tag= ak /*tag= ak /standard_name= "Single nucleotide polymorphism" 83040	/*tag= aj /*tag= aj /standard_name= "Single nucleotide polymorphism" 81378	<pre>/*tag= ai /standard_name= "Single nucleotide polymorphism" angle</pre>	<pre>/*tag= ah /standard_name= "Single nucleotide polymorphism" 80090</pre>	/*tag= ag /*tag= ag /standard_name= "Single nucleotide polymorphism" 79208	/*tag- /*tandard_name= "Single nucleotide polymorphism" 75770	<pre>/*tag= ae /standard_name= "Single nucleotide polymorphism" 74237</pre>	/*tag= ad /#tagdard_name= "Single nucleotide polymorphism" 73664	/*tag= ac /*tag= ac /standard_name= "Single nucleotide polymorphism" 71037	<pre>/*tag= ab /standard_name= "Single nucleotide polymorphism" 70818</pre>	<pre>/*tag= aa /standard_name= "Single nucleotide polymorphism" 70637</pre>	/*tag= z /standard_name= "Single nucleotide polymorphism" 64676	/*tage y /*tandard_name= "Single nucleotide polymorphism" 64350	/*tag= x /*tag= x /standard_name= "Single nucleotide polymorphism" 60910	/*tag= w /*tandard_name= "Single nucleotide polymorphism" 54446	1/040 /*tag= v /standard_name= "Single nucleotide polymorphism"	<pre>/*tag= u /standard_name= "Single nucleotide polymorphism"</pre>	<pre>/*tag= t /standard_name= "Single nucleotide polymorphism" 46771</pre>	/*tag= s /standard_name= "Single nucleotide polymorphism" 46553	/*tag= r /standard_name= "Single nucleotide polymorphism" 46172	41614 /*tag= q /standard_name= "Single nucleotide polymorphism" 45740
Qy 84 CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143	Query Match 37.5%; Score 149.8; DB 14; Length 151909; Best Local Similarity 71.0%; Pred. No. 5.2e-31; Matches 211; Conservative 1; Mismatches 83; Indels 2; Gaps 1;	/standard_name= "Single nucleotide	variation 122339	FT variation 120523  FT Variation 120523  FT Variation 120527	variation /standar	/standar variation 118132 /*tag=	FT variation 117729  FT variation 17729  FT /*tag= bf	2 6	variation /standau /standau /*tag-	/standar variation 110420 /*tag=	variation /*tag=	variation /standard	variation /standar /*tag=	variation	variation 103205	variation 102545	21	/*tag= /standar variation 98461	variation 97080	/standard variation 96770 /*tag= a	variation 96522	variation 95692	ard

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RESULT 32
ACN44170
                                                                                                                                                                               The present invention relates to novel DNA and protein sequences which care associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for a bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (carcinoma; or arcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent (US2002182586A1, for which no sequence data was published
Matches 196; Conservative
                                                              Query Match
                                                                                                                                 Sequence 196686 BP; 53978 A; 42758 C; 43862 G; 55372 T; 0 U; 716 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 484; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morris DW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
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                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-328604/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAG--TGAGCT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATGGTGGCATGTGCCTATAATCCCAGCTACTTGGGAAGCTGAGGCAGGAGAATCGCTT
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                                 Score 149.8;
Pred. No. 5.7
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   Mismatches
                                    .7e-31;
                                                                  DB 11;
      58;
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      Indels
                                                              Length
                                                                     196686;
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      Gaps
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81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140

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ARESULT 33
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ARESTATA
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27-SEP-2000;
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29-SEP-2000;
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25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
22-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL65836 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAATAGC
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2000US-0209531P

2000US-0233617P

2000US-0234009P

2000US-0234053P

2000US-0234053P

2000US-0234953P

2000US-0234953P

2000US-0234923P

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2000US-0234923P

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reoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in cy expression is indicative of anti-neoplastic activity. (I) has cytostatic gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producting a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
03-0CT-2000;
03-0CT-2000;
03-0CT-2000;
03-0CT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 4173; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for anti-neoplastic agent involves exposing cells to a agent to be tested for anti-neoplastic activity, and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-188264/24
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DR,
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                                                                                                                                                                                                                            GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                                                                                                     AAGACCAGTCTGGCCAACATGGTGAAACCCCCGCCTCTACTAAAAATACAAAAATTAGCTG
                                                                                                                                                                                                                                                                                                                   GAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5670 BP;
                                          GTCTCAAAAACAACAACAAAAACAAAA 344
                                                                                          TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT
                                                                                                                                         AGATCGCAGAGTGAGCCGAAATCACAGATC----ACAGAGTGAGCAGAGTGAGACKCC
                                                                                                                                                                                         GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
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GTCTCARAAAAAAAAAAAAAAAAAAAA 5040
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12000US-0237274B.
12000US-023729S.
12000US-023729S.
12000US-023742SP.
12000US-023742SP.
12000US-0237606P.
12000US-0237606P.
12000US-0244867P.
12000US-0245084P.
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75.0%;
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Pred. No. 2.2e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel reagent for diagnosis, molecular CC definition and therapy of chronic inflammatory joint diseases, and other CC inflammatory disorders, infective or tumour diseases in humans. The CC products of the invention have antiinflammatory, cytostatic, antirheumatic and immunosuppressive activity and can be CC used for gene therapy. The reagent of the invention and any proteins and CC extractive derived from it, are used (i) for analysing tissue and blood samples for medical diagnosis; (ii) for diagnosis and characterisation of CC chronic joint diseases, on the basis of molecular characterisation, and CC extraining the etiological pathogenicity principle of as yet cuncharacterised inflammatory diseases, also monitoring progression and/or CC treatment of disease, and optimisation of therapy and (iii) for CC treatment of disease, and optimisation of therapy and (iii) for CC treatment of disease, and optimisation of therapy and (iii) for CC treatments for inflammatory diseases, particularly of joints, confections and tumours. ACA64801-ACA64965 represent human polynucleotides of used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5670 BP; 1267 A; 1630 C; 1616 G; 1157 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2001; 2001DE-01027572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chronic inflammatory joint disease; infection; tumour; antiinflammatory; cytostatic; antiarthritic; antirheumatic; immunosuppressive; gene therapy; etiological pathogenicity; ds
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                                   TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 5068
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GTCTCAAAAACAACAACAAAAAAAACAAAA 344
                                                                                                                                                                                      AAGACCAGTCTGGCCAACATGGTGAAAACCCCCGCCTCTACTAAAAATACAAAAATTAGCTG
                                                                                                                                                                                                                                                            GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC
                                                                                                                                                                                                                                                                                                 GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
                                                                      AGATCGCAGAGTGAGCCGAAATCACAGATC----ACAGAGTGAGCAGAGTGAGACKCC 316
                                                                                                           GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
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75.0%;
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Pred. No. 2.2e-31;
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ARESULT 35
ARE74508/c
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gene;

WPI; 2006-145797/15 Segman R, Shalev A, Goltser T, Friedman N, Shefi N, Kaminski z

02-AUG-2004; 2004US-0592408P

YISSUM RES DEV CO HEBREW UNIV JERUSALEM. HADASIT MEDICAL RES SERVICES & DEV LTD.

New kit comprising 10 and no more than 574 polynucleotides capable specifically binding at least one specific polynucleotide sequence, useful for determining predisposition of a subject to develop PTSD, for diagnosing PTSD. of. or

ID NO 22; 157pp; English.

The invention relates to a kit for determining predisposition of a cubject to developing post-traumatic stress disorder (PTSD) comprising at least 10 and no more than 574 polynucleotides, where each of the comprising the composition of a composition of the polynucleotides is capable of specifically binding at least one specific polynucleotides is capable of specifically binding at least one specific cited comprising the polynucleotides cited, and a microarray comprising cited comprising the polynucleotides cited, and a microarray comprising considered comprising the polynucleotides cited, and a microarray comprising considered comprising the polynucleotide sequence. The kit comprises each of the polynucleotide sequence is specifically binding at least one specific colored modern and an RNA molecule. Each of the polynucleotides is at least one colored and no more than 50 nucleic acids in length. Each of the polynucleotides is at least one reagent considered for detecting hybridization of the polynucleotides and at least one reagent constable for detecting hybridization of the polynucleotides and at least considered in the subject to developing properties at least one reagent considered in length. Each of the polynucleotides and at least considered in the subject to developing properties at least one reagent and instructions for using the kit in determining predisposition of at least one gene as a comparation of the subject to developing properties and at least one capable of regulating an expression level of a medicament identified for compression of a modern considered considered considered specification, but the manufacture of the invention. Note: The sequence considered the polynucleotide of the polynucleotide sequence. data for this patent did not form part of the printed specification, was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. but

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Sequence 5670 BP;
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Matches 201; Conserv
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07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
14-JUL-2000
26-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                      Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease;
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04-FEB-2000;
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          14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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19-MAY-2000;
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCTCAAAAAAAAAAAAAAAAAAAAAA 5040
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        2000US-0190076P.
2000US-0205515P.
2000US-0209467P.
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2000US-0216480P.
2000US-0217487P.
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2000US-0217496P.
2000US-0224518P.
2000US-0224518P.
2000US-0225214P.
2000US-0225214P.
2000US-0225266P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                    2000US-0189874P
                                                                                                                                                                                                                                              2000US-0184664P
2000US-0186350P
                                                                                                                                                                                                                                                                     2000US-0180628P
                                                                                                                                                                                                                                                                               2000US-0179065P
                                                                                                                                                                                                                                                                                                                                                                                            disorder; Meckel's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 149.6;
Pred. No. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NO:
                                                                                                                                                                                                                                                                                                                                                                                                      appendicitis; chronic colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5670;
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Best Local Sin
Matches 200;
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08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
17-NOV
                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders digestive system, particularly cancer and cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                              5540
                                                                                                                                  5600
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                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN GENOME
                                                                                                                            ATGCCTGTAATCCCAGCACTTTGGAAGGCCAAGGCGGGTGGATCACCTGAGGTCAGGAGT
                                                                                                                                                      ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
                                                                                                                                                                                                                                                                                                  8205
    TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                  TCGAGACCATCCTGGCCAACATGGTGAAACCCCGGTCTTTACTAAAAAATACAAAAAAATAGC
                                            TCGAGACCAGCCTGGCAAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                              37.3%;
ilarity 75.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
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2000US-024920PP.
2000US-0249210P.
2000US-0249211P.
2000US-0249211P.
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2000US-0249211P.
2000US-024921P.
2000US-02592P.
2000US-0251868P.
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2000US-0246609P.
2000US-0246610P.
2000US-0246611P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                986pp; English.
                                                                                                                                                                                                           Score 149; DB 4; I
Pred. No. 3.6e-31;
1; Mismatches 56;
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01-SEP

2000US-0225447P.
2000US-022575PP.
2000US-022575PP.
2000US-022575PP.
2000US-022575PP.
2000US-0226681P.
2000US-0226681P.
2000US-022687P.
2000US-022934P.
2000US-022934P.
2000US-022934P.
2000US-023934P.
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2000US-0231243P.
2000US-0231239P.
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2000US-0231239P.
2000US-0231239P.
2000US-023123P.
2000US-02312

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ARESULT 37
ARISOLT 37
ARISOLT AN ARISOLE ANA ARISOLE AN ARISOLE ANA                                                                                                                                                                                                                                                                                                                                                          01-SEP-2000

06-SEP-2000

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11-NO
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antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001.
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUL-2000;
                                                                                                                        (HUMA-) HUMAN
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2000US-020551SP.
2000US-0216880P.
2000US-0216880P.
2000US-0225447P.
2000US-0231243P.
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2000US-0249211P.
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2000US-0251030P.
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2000US-0246526P.
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                                                                                                                            GENOME SCI INC
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The invention relates to novel genes (AAI62752-AAI62961) and proteins CC (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CThe nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, by preast, gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic consemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, allergies, autoimmune haemolytic considerations schematoid arthritis and ulcerative colitis; (c) CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) CC cardiovascular diseases e.g. cerebral anoxia and epilepsy; and (f) CC infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly constructed and the format directly constructed and the format directly constructed specification, but was obtained in electronic format directly constructed specification, but was obtained pot sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the including cancer, immune response and neuronal disorders.
                                                          Sequence 8205 BP; 2216 A; 1646 C; 1763 G; 2580 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 276; 532pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-476225/51.
   DB 4;
Length 8205;
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밁 Ś 밁 Ś 밁 Ś B Ś 밁 á Matches Query Match Best Local 5368 5420 5480 5540 5600 141 321 201 261 200; 81 Similarity ATGCCTGTAATCCCCAGCACTTCGGGAGGCCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA CAAGACTGC TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC ATGCCTGTAATCCCAGCACTTTGGAAGGCCAAGGCGGGTGGATCACCTGAGGTCAGGAGT САЛАЛАСЛАСЛАСАЛАЛАСАЛАЛА 345 TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320 CGGGTGTGGTGTGCGCCTATAATCCCAGCTACTCAGGAGGCAGAGGTTGCAGTGAGC 37.3%; nilarity 75.5%; Conservative -GCCATTACACTCCGGCCTGGGCAACAAGAGCAAAACTCCATCT 1; Score 149; Pred. No. 3. Mismatches .6e-31; 56; Indels 8 Gaps 140 5369 5421 5481 200 5541 260

ADO79404
ID ADO
XX
AC ADO
XX
AC ADO
DT 26-DT 26-CY
KW CYt
KW CYt
KW D4KW 281
KW 281
KW Chr
XX
KW Hom
OS Hom
OS Hom
VAIR
FT VAIR RESULT 38 CENPC1; gene; ds; SNP; single nucleotide polymorphism; D4, zinc and double PHD fingers, family 3; CERD4; cer-d4; FLJ14079; 2810403B03Rik; Rho family guanine-nucleotide exchange factor; chromosome 14q24.3-q31.1. Cytostatic; Gene therapy; breast cancer; DPF3 region, 26-AUG-2004 ADO79404 standard; Homo sapiens SEQ ID 3. (first entry) Location/Qualifiers DNA; 89900 human; DLG1; KIAA0783; DPF3;

CA.

Barash

Ruben

variation

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מ יייי איני איני איני איני איני איני אינ	r xrd_name= "Single nucleotide polymorphism" "This SNP is described as a T/C SNP"	= q dard name= "Single nucleotide polymorphism" = "This SNP is described as a A/C SNP"	/*tag= p FT /*tag= p FT /*tag= p FT /*standard name= "Single nucleotide polymorphism" /*This SNP is described as a T/C SNP" 32003	/*tag= o	n ard name= "Single nucleotide polymorphism" "This SNP is described as a A/G SNP"	/*Trage m FT /*tage m FT /*tag	= 1 dard_name= "Single nucleotide polymorphism" = "This SNP is described as a G/A SNP"	<pre>- k dard name= "Single nucleotide polymorphism" - "This SNP is described as a G/A SNP"</pre>	/*Cage ] FT /*Cage ] FT /*Standard_name= "Single nucleotide polymorphism" FT /note= "This SNP is described as a T/C SNP"  FT 24582 FT	1 ard name= "Single nucleotide polymorphism" "This SNP is described as a A/G SNP"	h hard name= "Single nucleotide polymorphism" "This SNP is described as a G/C SNP"	= 9 dard name= "Single nucleotide polymorphism" = "This SNP is described as a A/T SNP"	/*tag= f FT /*tag= f FT /*tag= f FT /*standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a C/G SNP"  18561 FT FT	= e dard_name= "Single_nucleotide_polymorphism" = "This_SNP is_described_as_a_A/T_SNP"	d dard name= "Single nucleotide polymorphism" = "This SNP is described as a T/C SNP"	ag= c andard name= "Single nucleotide polymorphism" te= "This SNP is described as a A/G SNP" 81	/*tag= b FT /*tag= b FT /*tag= b FT /standard name= "Single nucleotide polymorphism" FT /note= "This SNP is described as a T/G SNP" FT 9719	a rd name= "Single nucleotide polymorphism" "This SNP is described as a A/C SNP"
AUTTOCTOL		variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	variation .	variation	variation	variation	variation
/*tag= ak /*tag= ak /standard_name= "Single nucleotide polymorphism"	<pre>/*tag= aj /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/C SNP" 72720</pre>	, E	/ ray / standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/C SNP" 60682 /*tag= ai	, H	/standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/C SNP" 53971 /*tag= ag	_ 22	. A	= #	<pre>/standard_name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/G SNP" 49774 /*tag= ac</pre>	"Single nucleotide P is described as a	/standard_name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/G SNP" 43090 /*tag= aa	/standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a A/C SNP" 42799 /*tag= z	/*Cag= x /standard_name= "Single nucleotide polymorphism" /note= "This SNP is described as a G/C SNP" 42593 /*Fag= v	= K	/'cray= v /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a G/A SNP" 40033	- 22	/*Lag= t /standard name= "Single nucleotide polymorphism" /note= "This SNP is described as a G/A SNP" 36254	<pre>/standard_name= "Single nucleotide polymorphism" /note= "This SNP is described as a T/C SNP" 35856</pre>

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RESULT 39
AREP92655/c
ID AREP926
XX AREP926
XX OREP926
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Diagnosis; ss; gene; neurodegenerative disease; Alzheimers disease;
                              Human Ras effector protein Rin3, cDNA
                                                                  20-APR-2006
                                                                                                 AEF92655
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24-JUL-2003;
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CC neurodegenerative disease progression in a subject, identifying a risk concerned to a neurodegenerative disease in a test subject, identifying a risk controlled to a neurodegenerative disease in a test subject, identifying a risk controlled to a neurodegenerative disease in a test subject, a solid support comprising one or more biomarkers, where the biomarker is one or more proteins comprising HSP60, Dihydrollpoamide dehydrogenase, ER-60 cromprising comprising HSP60, Dihydrollpoamide dehydrogenase, ER-60 cromprising comprising HSP60, Dihydrollpoamide dehydrogenase, ER-60 cromprising comprising HSP60, Prohibitin, Phosphoglycerate muttase 1, comprising neroxidaes B, RAS-related protein RAP1B, cromprising cromprising cromprising cromprising cromprising cromprising cyclin D1, cyclin B, cromprising cromprising cyclin D1, cyclin B, cromprising cyclin G1, weel, hTR2, CDC25b, GSK3 beta, protein kinase C alpha, C5, C1 contichymotrypsin, HSP 27, HSP 90, crystalline, GAPDH, ferritin H, cox 1, cox 2, transferrin, or its combinations). The curodegenerative disease, screening a therapeutic agent for treating a remonstering a neurodegenerative disease.
                           Query Match
Best Local Similarity
                                                                                                                                                                                                                      progression monitoring a response to a neurodegenerative disease treatment, identifying a risk for a neurodegenerative disease, and differentially diagnosing a neurodegenerative disease, e.g. Alzheimer's disease and Parkinson's disease, in a test subject. The present sequence is a cDNA for a human biomarker, used in a microarray in the method of the invention. NOTE: The specification describes AEF92574-AEF92813 (table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disease treatment, identifying a risk for a neurodegenerative disease, and differentially diagnosing a neurodegenerative disease in a test subject. Also included are diagnosing a neurodegenerative disease in a subject, screening for a therapeutic agent for the treatment of a neurodegenerative disease, monitoring a agent for the treatment of a neurodegenerative disease, monitoring a
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neuroprotective; nootropic; antiparkinsonian; screening; prog
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RESULT 41
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Best Local S
Matches 207
  The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are
                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               granulocyte activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ds; granulocytic cell; DNA chip; bacterial infectio viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA differentially expressed in granulocytic
                                                                                                                                                                                                                                                                                                                                                       Beazer-Barclay
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Pred. No. 1.1e-30;
1; Mismatches 61;
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RESULT 42
ADA02774/c
ID ADA027
XX ADA027
XX ADA027
XX O6-NOV
XX VX Human
XX Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 229;
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Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
                                                                         Human ARHGEF1 carcinoma associated gene, SEQ ID NO:1292
                                                                                                                                                   06-NOV-2003 (first entry)
                                                                                                                                                                                                                                 ADA02774
                                                                                                                                                                                                                                                                                                   ADA02774 standard; DNA; 44075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (ADA)1482-ADA)3094), and to CC carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogenes or CC pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host CC protococogenes. The CA nucleic acid sequences can be used to diagnose CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular CC tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The CC genence of the invention. Note: The complete sequence data for this complete.
                                                                                                                                                                                                                                                                                                                                                                               Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44075 BP; 8314 A; 11402 C; 11137 G; 8371 T; 0 U; 4851 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1292; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-587068/55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY
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                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                     GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
    GTCTCAAAAACAACAACAAAAAAAACAAA 343
                                                                                                                                                                   GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                              AAGACCAGTCTGGCCAACATGGTGAAAACCCCCGCCTCTACTAAAAAATACAAAAATTAGCTG
                                                                                                                                                                                                                                                                                                                                        GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
                                           TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 842
                                                                                    AGATCGCAGAGTGAGCCGAAATCACAGATC-----ACAGAGTGAGCAGAGTGAGACKCC 316
                                                                                                                              GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT 8486
                                                                                                                                                                                                                                                                                               GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                37.2%;
                                                                                                                                                                                                                                                                                                                                                                               1;
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Pred. No. 7.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
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RESULT 43
ADB72512;
ID ADB72512;
XX ADB72512;
XX ADB72512;
XX DE Human ARHGEF1 gene.
XX human; ds; cytostatic; gene ther cancer; neoplasm; adenocarcinoma XX Homo sapiens.
XX WO2003008583-A2.
XX WO2003008583-A2.
XX WO2003008583-A2.
XX BD 30-JAN-2003.
XX 26-DEC-2001; 2001WO-US051291.
XX 27 30-JAN-2003; 2001WS-00052482.
PR 23-OCT-2001; 2001US-00052482.
PR 23-OCT-2001; 2001US-00052482.
PR 23-OCT-2001; 2001US-00052482.
PR 23-OCT-2001; 2001US-00034650.
XX (SAGR-) SAGRES DISCOVERY.
XX (SAGR-) SAGRES DISCOVERY.
XX (SAGR-) SAGRES DISCOVERY.
XX New recombinant nucleic acid, usperior cancers, neoplasm, adenocarcinom XX (SAGR-) saccombinant nucleic acids and poch carcinomas, e.g. lymphomas, cancer carcinomas, e.g. lymphomas, cancer cancer cancer sarcomas. The present sequence rocce cancer sarcomas. The present sequence rocce rocce rocce rocce sarcomas. The present sequence rocce rocce rocce rocce rocce sarcomas. The present sequence rocce                                                                                         유 성 유 성
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Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancers, neoplasm, adenocarcinoma, or sarcomas.
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neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                           GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 340; 2304pp; English.
                                       GTCTCAAAAACAACAACAAAAAAAAAAAA 343
                                                                                                                                                         AGATCGCAGAGTGAGCCGAAATCACAGATC-----
                                                                                                                                                                                                                  GGCATGGTGGCAGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
                                                                                                                                                                                                                                                     GGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                                                                                                                                               AAGACCAGTCTGGCCAACATGGTGAAACCCCCGCCTCTACTAAAAAATACAAAAATTAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 7.7e-31;
1; Mismatches 60;
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8399
                                                                                                                                                               ACAGAGTGAGCAGAGTGAGACKCC
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RESULT 44
ADC85254/c
ID ADC852
XX ADC852
XX ADC852
XX ADC852
XX Y
XX Human
XX Cytost
XX Homo s
XX Homo s
XX Homo s
YX W02003
XX O2-DEC
XX O2-DEC
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XX W0215
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC85254 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant nucleic acid comprising a nucleotide sequence the carcinoma-associated (CA) genes, useful for screening for candidates for diagnosing or treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-2002; 2002WO-US038582
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                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                 GAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAAATAGCTG
                                                                                                                                                                                                                                                      GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 40; 983pp; English.
                                                                                                                                                                                                                                                                                                                                                          44075 BP; 8314 A; 11401 C; 11138 G; 8371 T; 0 U; 4851 Other;
GTCTCAAAAAAAAAAAAAAAAAAA
                                                                                                                   ĠĠĊĂTĠĠŢĠĠĊĀĠĠĊĠĊĊŢĠŢĂĂŢĊĊĊĀĠĊŢĀĊŢŢĠĠĠĀĠĠĊŢĠĀĠĠCĀĠĠĀĠĀATCGCT
                                                                                                                                               GGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG
                                                                                                                                                                              AAGACCAGTCTGGCCAACATGGTGAAACCCCCGCCTCTACTAAAAATACAAAAATTAGCTG
                                                                                                                                                                                                                                        GCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGTGGATCACCTGAGGTCAGAGGTTC
                             GTCTCAAAAACAACAACAAAAAAAACAAA
                                                         TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT
                                                                                    AGATCGCAGAGTGAGCCGAAATCACAGATC----
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                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                            37.2%;
74.9%;
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                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                              Score 148.6; DB 1
Pred. No. 7.7e-31;
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; carcinoma-associated
 8399
                             343
                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                   60;
                                                                                       -ACAGAGTGAGCAGAGTGAGACKCC
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                            Length 44075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of any
drug
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RESULT 45 ADM74369/c

ADM74369 standard; DNA; 44075 BP

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cq neutralising the effect of a CAP and a method of diagnosing carcinoma or propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a cell sample from the patient and determining alterations in the cell sample from the patient and determining alterations in the cell sample from the patient and determining alterations in the cell sample from the patient and determining the nucleotide sequence. A compression of a first individual and comparises determining the expression of cell consecutions comprises determining the expression of the gene from type of a first individual and comparing the expression of the gene from the second normal tissue type from the first individual or a second unaffected individual, where a difference in the expression indicates that the first individual has carcinoma. A method of inhibiting the activity of a CAP comprises binding an inhibitor to the CAP. Treating carcinomas comprises administering to a patient an inhibitor of CAP. CC the nucleic acid. It comprises contacting an agent specific for the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. The nucleic acids are useful for preparing a composition for diagnosing or treating carcinoma e.g., classical ted (CA) nucleic acid of the invention. Note: The sequence data contained associated (CA) nucleic acid of the invention. Note: The sequence data contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to new recombinant nucleic acids. The invention also relates to a host cell comprising a recombinant nucleic acid or expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, method of screening for a bioactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  method of screening for a bioactive agent capable of modulating the activity of a CAP, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting the activity of a CAP, a method of treating carcinomas, a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                     seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 40; 29pp; English.
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02-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; carcinoma associated nucleic acid; CA nucleic acid; gene; carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human carcinoma associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORRIS D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engelhard
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2001US-00798586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic
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Query Match

37.2%;

Score 148.6;

DB 12;

Length 44075,

Sequence 49745 BP; 10151 A; 14745 C; 14496 G;

10151 T; 0 U;

202 Other

Sequence 44075 BP; 8314 A; 11402 C; 11137 G; 8371 T; 0 U; 4851 Other

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RESULT 46
ACN45134
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                         are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-328604/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACN45134 standard; DNA; 49745
                                                                                                                                                                                                                                                       The present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                            Recombinant nucleic acid useful for diagnosis and treatment comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003073826-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genomic sequence hCG31443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGACCAGTCTGGCCAACATGGTGAAAACCCCCGCCTCTACTAAAAATACAAAAATTAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTCAAAAACAACAACAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 8426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCATGGTGGCAGGCGCCTGTAATCCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma; lymphoma; cancer;
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                                                                                                                                                                                                                                                                                      ID NO 1930; Opp; English.
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RESULT 47
AESO4996_2
Continuation (3 of 5) of WP Sequence split into 5
WP Eragment Name
WP AEE04996_0
WP AEE04996_1
WP AEE04996_2
WP AEE04996_3
WP AEE04996_3
WP AEE04996_4
RESULT 48
AAD54538
ID AAD54
XX AAD54
XX AAD54
XX DT 26-JU
DT 26-JU
DX Humar
XX Humar
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Best Local Simi
Matches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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Human; p53 pathway; phosphatidylinositol biphosphate; PIB; therapeutic;
                            Human phosphatidylinositol biphosphate (PIB) DNA #1.
                                                           26-JUN-2003
                                                                                        AAD54538
                                                                                                                   AAD54538
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AEE04996 0
AEE04996 1
AEE04996 2
AEE04996 3
AEE04996 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTTAGCAGCCAGGCCAGGAGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCT
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                                                                                                                                                                                                                                                   CTTGAACCCAGGAGGCAGAGGTTTAGTGCCATTGCACTCCAGCTTGGGCAACAGAGTGAG
                                                                                                                                                                                                                                                                                                                                                                      TGGAGACCAGCCTGGCCAACATGGTGAAACCCCGATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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                                                                                                                  standard;
                                                                                                                                                                                                            ACKCCGTCTCAAAAAACAACAACAAAAAAACAAAAAAAAACCATA 352
                                                                                                                                                                                                                                                                                TGAGATCGC-----AGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAG
                                                                                                                                                                                                                                                                                                                                    TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                                                                           ACTCCATCTTAAAAAAAAAAAAAAAAAAGAAAAGAAAACTTA 15092
                                                                                                                                                                                                                                                                                                             TGGGCGTGATGGCATGCACCTGTAATCCCCAGCTACTCGGGAGGCTGAGGTGGGAGAATTG
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                                                           (first
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                                                                                                                  DNA;
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Begin End
                                                           entry)
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73.3%;
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73.2%;
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200001
300001
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    Mismatches

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310000
410000
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RESULT 49 ADH76849 ID ADH76 XX

ADH76849

standard;

DNA;

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                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method of identifying candidate p53 pathway-modulating agents. The method involves screening for agents that modulate the activity of phosphatidylinositol biphosphate (PIB). The methods are useful for identifying candidate p53 pathway-modulating agents used as therapeutic targets for disorders associated with defective p53 function. They are also useful for modulating p53 pathway in a mammalian cell or for diagnosing or treating a disease associated with defective p53 function, e.g. cancers such as breast cancer, colon cancer, lung cancer or ovarian cancer. Sequences of the invention are useful for in vivo assays to test the activity of candidate p53-modulating agents or to assays to test the activity of pathway process such as apoptosis or cell proliferation. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2001; 2001US-0296076P
10-OCT-2001; 2001US-0328605P
15-FEB-2002; 2002US-0357253P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying candidate p53 pathway-modulating agents, useful as therapeutic targets for disorders associated with defective p53 f comprises screening for agents that modulate phosphatidylinositol biphosphate activity.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 133893 BP; 33343 A;
                                                                                                                                                                                                                                                                                                                                                                                                   sequence is human PIB DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2002; 2002WO-US017526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; apoptosis;
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                                                                                                                                                                                                                                                                                                           196;
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                                                           CTTAAACCTGGGAGGTGGAGGTTGTACCAAGCGGAGATCGTGGAGACAGAGCAGGCCCCT
                                                                                                                                                                                   TTGAAACCAGCCTGGCCAACATGGTGAAACCTCATCTCTACTAAAAATACAAAAATTAGC 127504
                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCGGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                ACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTCTGGAGT 127444
                                                                                                                                                                                                                                                                            ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                            TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
GTCTCAAAAAACAAAACAAAACCCCCAAAAAA
                              CAAAAACAACAAAAAAACAAAAAACCATAAGACA
                                                                                         TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                         TGGGTGTGGTGGCACACCTGTAGTCGCAGCTACTCCGGAGGCTGAGGCAGGAGAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                           Conservative
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70.8%;
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                                                                                                                                                                                                                                                                                                           Score 148.6; DB 9;
Pred. No. 1.1e-30;
1; Mismatches 80;
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                                                             /standard_name= "Single nucleotide polymorphism"
replace(103270,A)
/*Far=- -
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replace(98848,T)
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replace(97004,G)
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replace(96227,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "Single nucleotide polymorphism"
replace(95767,C)
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replace(103156,C)
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replace(96797,A)
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replace(95538,G)
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replace(91276,G)
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replace(99803,G)
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| cplace(99450,A)
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replace(91268,C)
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                                                                                                                                                            standard_name= "Single
eplace(100220,A)
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eplace(99142,A)
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ceplace(97723,T)
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RESULT 50 AAK79514 ID AAK79

AAK79514 standard;

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Best Local Similarity
Matches 221; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence comprising one or more of the nucleotide exchanges (SNP's) given in the specification and at least 8 bases of surrounding sequence of the MCHR1 gene. The composition has anorectic activity. The polynucleotide composition may be used in gene therapy to treat the disorders of the invention. The composition is useful for disgnosing obesity related to the presence of a molecular variant of the MCHR1 gene or a susceptibility to the disorder. The MCHR1 protein or polynucleotide is useful for preparing a medicament for treating or preventing obesity related to the presence of a molecular variant of the MCHR1 gene. This polynucleotide presence of a molecular variant of the MCHR1 gene. This polynucleotide represents the melanin-concentrating hormone receptor 1 locus clone of the invention. This sequence is not shown in the specification. It has been taken from the GenBank accession number Z86090 provided in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel diagnostic polynucleotide composit The polynucleotide composition comprises: a sequence encoding a polypeptide with defined sequences given in the specification; a secapable of hybridizing to a melanin-concentrating hormone receptor (MCHR1) gene; a polynucleotide encoding an MCHR1 polypeptide; or a melanin-concentration polypeptide; or a melanin-concentration of the metallic polypeptide                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 122557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      presence of a the disorder.
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                                                       AAAAACAACAACAAAAAAACAAAAAAA 347
                                                                                                                     GAACCCGGGAGGCAGAGGTTGCAGTGGGCCGAGATCGTGCCAAGAGTGAAACTCCCTCTC
                                                                                                                                                                                                                                                GCATGGTGGCAGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCTGGAGAATTGCTT
                                                                                                                                                                                                                                                                                                        GCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
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AAAAAAAAAAAAAGAAAGAAAGAAAA 68308
                                                                                                                                                                            GATCGCAGAGTGAGCCGAAATCACAGATCACAGA--GTGAGCAGAGTGAGACKCCGTCTC
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Pred. No. 1.2e-30;
1; Mismatches 102
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immune;   haematopoletic;   immune/haematopoletic antigen; cance tatic; gene therapy; vaccine; metastasis; ds.  G-2001.  N-2001; 2001WO-US001354.  N-2001; 2001WO-US001354.  N-2000; 2000US-019662BBB-B-2000; 2000US-0198123B-2000; 2000US-019812B-2000; 2000US-019812	07-NOV-2001 (first entry)
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2000US-023499RP 2000US-023499RP 2000US-0235934P 2000US-0235934P 2000US-0235934P 2000US-0235937P 2000US-0235368P 2000US-0235368P 2000US-0235368P 2000US-0235368P 2000US-0235368P 2000US-0235368P 2000US-02353703P 2000US-023703P 2000US-023703P 2000US-023703P 2000US-02341785P 2000US-0241785P 2000US-0244617P 2000US-0244617P 2000US-0244617P 2000US-0244617P 2000US-0244617P 2000US-024461P 2000US-0244921P 2000US-024921P 2000US-02492P 2000US-02492P 2000US-02492P 2000US-024928P 2000US-02492P 2000US-0	000US-023306 000US-023306 000US-023421

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Séarch completed: July 17, 2006, 20:16:38
Job time : 542 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cq activity, and can be used in gene therapy and vaccine production. (I) cq proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For cq example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome cq that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) cq polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the cq protein. (I) proteins and polynucleotides may be used to prevent, cq diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic acids and aka64703 to AAK87694 represent human immune/haematopoietic acids and aka62169 represent sequences used in the exemplification of the present invention of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-2000; 2000US-0251869P.

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11-DEC-2000; 2000US-0254097P.

05-UAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9469 BP; 2940 A; 2203 C; 1941 G; 2385 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 34326; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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DB313291 DB313291
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BF965924 602277287
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R34561 y958h66 r1
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AA836548 G036h04.8
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Genomic survey sequence.

AQ416484

AQ416484.1 GI:4470608

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CA419549 UI-H-FH0-
AG179363 Pan trog1
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Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seg primer: SP6
Class: BAC ends.
  AQ936397

AQ936397

ACPT APCI-11-Seg1-4-200N9-T7 RPCI-11 Human segment 1-4 genomic library Homo sapiens genomic clone RPCI-11-Seg1-4-200N9-T7 similar to Human AQ936397.1 GI:6654471

GSS.
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Other GSSB: RPCI11-153H2.TV
Other GSSB: RPCI11-153H2.TV
Contact: Shaying Zhao, William Nierman,
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1:
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7558537"
/db_xref="taxon:9606"
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L; Mismatches
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Pred. No. 1.9e-19;
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                                                                                                                    617 bp oj49905.yl Human lacrimal gland, clone oj49905 5', mRNA sequence. CK430466
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osoegawa,K., Mammoser,A.G., Wu,C., Frengen,E., Zeng,C., Catanese,J.J. and de Jong,P.J.

A bacterial artificial chromosome library for sequencin complete human genome
Genome Res. 11 (3), 483-496 (2001)
                                                                                                                   clone oj49g05
CK430465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: pdejong@mail.cho.org
BAC end sequences. For clone availability please contact
Jong (pdejong@.mail.cho.org). BACPAC Resources WWW site:
www.chori.org/bacpac
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747 Fifty second Street, Oakland, CA
Tel: 510 450 7911
Pax: 510 450 7924
                                                   Homo sapiens
                                                                                                CK430465.1 GI:40678584
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                                                                 Homo sapiens (human)
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/clone_lib="RPCI-11 Human segment 1-4 genomic library"
/note="Vector: pBACe3.6; BAC clones in E. coli DH10B"
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AGENCOURT 10405312 NIH MGC_82
5', mRNA sequence.
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Ozyildirim,A.M., Wistow,G.J., Gao,J., Wang,J., Dickinson,D.P.,
Prierson,H.P. Jr and Laurie,G.W.
The lacrimal gland transcriptome is an unusually rich source of
rare and poorly characterized gene transcripts
Invest. Ophthalmol. Vis. Sci. 46 (5), 1572-1580 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: graeme@helix.nih.gov
Plate: 49 row: g column: 0:
Seq primer: M13RP1 reverse p:
Location/Qualifiers
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Fax: 301 496 0078
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/note="Organ: Eye; Vector: pcMvSport6; RNA was extracted
from 2 human lacrimal glands. A directionally cloned cDNA
library in the pcMvSpORT6 vector(Life Technologies) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's Instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adapter
[5'.pgACTAGTTCTAGATCGGACCGCCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
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/dev_stage="Adult"
/lab_host="EMDH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                 sequence.
                                             AA405549 as/ pp mkwa
zw39f03.rl Soares total fetus ND2HF8 9w
IMAGE:772445 5' similar to contains Alu
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fominidae; Homo.
                                                                                                                                                                                                                                                                                     GATCGCAGAGTGAGCCGAAATCACAGAGTCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                        AGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCCGATCACCTGAGGTCAAGAGATCG
                                                                                                                                                                                                                       AAACAACAACAAAAAAAAAAAAAAACCATAAGACATT 359
                                                                                                                                                                                                                                                       GCTCGCA-----CCATTGCACTCCAGCCTGGGTGAAGAGCGAGACTCTATCTCAA
                                                                                                                                                                                                                                                                                                                                 GCATGGTGGCATGTGCCTGTAATCCCAGCTACCGAGGAGGCAGAGGCTGCAGTGAGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                      AGACCAGCTTGGCCAACATGGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGTAATCCCAGCACTTTGGGAAGCCGAGGAGGGCGGATCACCTGAAGTCAGGAGTTTG
                                                                                                                                                                                    AAAATAAAAAAAGTAAAATAAATAAATAAAAT 282
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/db_xref="taxon.9606"

/clone="IMAGE:6615547"

/lab host="PH10B (T1 phage-resistant)"

/lab host="PH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_82"

/note="Grgan: testis; Vector: pDNR-LIB (Clontech); Site_1:

/fil (ggccgctcggco); Site_2: Sfil (ggccattatggco); 5' and
3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCGGCCACTG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size

1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained

inserts by PCR. This library was enriched for full-length

inserts by PCR. This library was enriched for full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clones and was constructed by Clontech Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 151.2; DB 3; Pred. No. 3.9e-19;
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                                                       Homo sapiens cDNA clone repetitive element;, mRI
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RC2-H70252-120200-014-c06
BE149224
BE149224.1 GI:8611948
EST.
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Allen, M., Bowles, L., Dubuque, T., G
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.
Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.
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                                        GCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCA 270
                                                                                                                             CTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTG
                                                                                                                                                                                               CTCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGTTCAAGACTAGC
                                                                                                                                                                                                                                             CCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATC
                                                                                                                                                                                                                                                                                              AATCCGGAGATAAAGAAATTGAGGCATGAATTGGCTGGGCACGGTCGTCACGCCTGTAAT 228
                                                                                                                                                                                                                                                                                                                                            AACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAAT
GCATGCACCTGTAATCCCGGCTACTCGGGAGGCTGAGGTTGCAGTGAGCCAAGATTGCA
                                                                                              CTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAATGAGTTGGGCATGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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'lab_host="DH10B"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                            Score 151; DB 1
Pred. No. 5e-19;
0; Mismatches
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,N., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 357;
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M., Martin,J
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401 bp mR1 HT0252 Homo

sapiens cDNA,

EST 21-JUN-2000 mRNA sequence.

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RESULT 7
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-HT0252-120
200-014-c06&t3=2000-02-12&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                               AGATCGCACTACTGCACTGCACTCCAGCCTGGGTGA-CAGAGCAAGACACTGTCTCA
                                                                                                                                                                                 AGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCA
                                                                                                                                                                                                                      GGCGTGGTGGCGTGCACCTGTAATCCCAGCTACTCAGGAGGCAGAGGTTGCAGTGAGCCA
                                                                                                                                                                                                                                                   GGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGGAGATTGCAGTGAGCTG
                                                                                                                                                                                                                                                                                               AGACCAGCCTGGCCAACATGTGTAAAACCCCCGTCTCTACTAAAAATACAAAATTAGCCA
                                                                                                                                                                                                                                                                                                                                 AGACCATCCTGGCCAACATG-GTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTG
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                                                                        AAAACAAACAAACAAAAAAACAGA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo gapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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197; Conser
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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17000600002901 GRN_PREHEP
CN272188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rbrandenberger@geron.com
Insert Length: 513 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 Constitution Drive, Menlo Park, CA 94025, USA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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  AAAAACAAAACAAACAAACAAACAAAAAAAAACAAC 326
                                     CAAAAACAACAACAAAAAAACAAAAAAACCATAAGAC 356
                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="CRM_PREHEP"
/noce="Oligo dT primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="embryonic stem cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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71.48;
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Pred. No. 8.6e-19;
D; Mismatches 79
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sapiens cDNA 5', mRNA sequence.
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CZ455807 613 bp DNA MCF738H04TF Human MCF7 breast cancer cel Homo sapiens genomic clone MCF7_38_H04,

cell line library 04, genomic survey

GSS 20-OCT-2005

(MCF7

Homo sapiens (human)

GI:77932102

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VERSION
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AUTHORS
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SOURCE
ORGANISM
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DB313291/c
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                                             sequence.
DB313291
DB313291.1
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Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
               Homo
                                                                                               DB313291 542
DB313291 CTONG2 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: svolik@cc.ucsf.edu
This clone is available from Amplicon
                                EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Volik SV
Colin Collins' lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                          CAAAAACAACAACAAAAAACAAAAAA 346
                                                                                                                                                                                                                                                                                                   TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                          TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
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Box 0808, San Francisco,
415 502 7066
415 502 5665
sapiens (human)
sapiens
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/db_xref="taxon:9606"
/clone="MCF7_38_H04"
/sex="female"
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Francisco, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 149.6; DB 1
Pred. No. 8.3e-19;
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RESULT 10
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RPCI-11-343C15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-343C15, genomic survey sequence.
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Yanashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Kushida, N., Ishi1, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Murakawa, K., Ishidaa, S., Ishibashi, T., Takahashi-Fujii, A., Mayai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
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Mammalia; Eutheria;
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2-6-7 Kazusa-Kamatari, Kisarazu,
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                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTGTAATCCCAGCACTTTGGNAGGCCAAGGCTGGCAGATCACTTGAGGTCAGGAGTTC
                                                                                                                                                                                                                                                                                                                                               AGATTGCGCCACTGCACTCCAGCCTGGGCGACACACTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGTGGTGGCACATGCCTGTAGTCCCAGCTATTTGGGAGGCTGAGGCTGCAGTGAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CTONG2000516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="tongue, tumor tissue'
clone_lib="CTONG2"
                                                                                                                               GI:4871776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.2%;
79.5%;
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Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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292-0818,

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RESULT 11
DA572262/c
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                                                                            VERSION
KEYWORDS
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                                                                                                                                                      DEFINITION
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Matches
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                                         ORGANISM
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                                                                                                              Bequence.
DA572262
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Zhao,S.,
Venter,J.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                  DA572262
DA572262 HEMBB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_GSS8: RPCI-11-343C15.TJ
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
                                                                            DA572262.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq_primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map Building
                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGGCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                                                                                                               AAAAAAAAAGAAAAGAAAAGAAAAGAAAACATACACTGAAATTTTAGGGGT 166
                                                                                                                                                                                                                                                                                                                                                                        GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                            GCGTGGTGGTGGGTGCCTGTAATCCCAGCTACTCGAGAGGCAGAGGTTGTAGTGAGC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACCAGCCTGGCCAACATGGTGAAAACCCCCATTTCTACTAAAAATACAAAAATTAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAATAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to
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of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                    -CAAGATTGCACCACTGCACTCCAGTCTGGGCGACAGAGTGAGACTCCATCTCAA
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Adams,M.D., Nierman,W., Malek,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male_BAC_Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7631390"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
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72.1%;
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 148.4; DB 1
Pred. No. 1.4e-18;
1; Mismatches 72
                                                                                                                                                  cDNA
                                                                                                                                                    clone
                                                                                                                                                                     mRNA
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                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                        Euteleostomi;
                                                                                                                                               EST 07-NOV-2005
2 5', mRNA
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AG170656/c
                                                                            VERSION
KEYWORDS
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PUBMED
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                                         ORGANISM
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                                                                          Pan troglodytes 1
sequence.
AG170656
AG170656.1 GI:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Ison, T., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department
Virology, Institute of Medical Science, University of Tokyo, and
     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                        Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                         Pan troglodytes (chimpanzee)
                                                                                                                                                                     AG170656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLJ Project (HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo
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                                                                                                                                                                                                                                                               AAAAAAAAAAAAA 283
                                                                                                                                                                                                                                                                                            AAACAACAACAAAA 337
                                                                                                                                                                                                                                                                                                                                    GATCACGCCACTGCTGCACTCCA-----GCCTGGGTGACAGAGTGAGACTCCATCACAA
                                                                                                                                                                                                                                                                                                                                                                        GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                            GCATAGTGGCACACGCCCATAGTCCCAGCTACTTGGGAGGCTGAGGTTGCACTGAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGACCAGTCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="HEMBB1"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole embryo, m
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="HEMBB1000862"
                                                                                               GI:16700334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.8%;
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                                                                                                                                                  DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Team)
   Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                    clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 148.4; DB 9
Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                     691
                                                                                                                                                  1 bp DNA RP43-039L04.TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mainly body"
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Indels Length

9

Gaps

847;

genomic

SS survey

09-JAN-2002

297

323 351 263

411 203 471 143

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RESULT 13
BF965924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama, A., Hattori, M. Totoki, Y., Watanabe, H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
                                                                                                                                         602277287F2 NIH_MGC_86 Homo
Hominidae; Homo
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                             Homo sapiens
                                                             Homo sapiens (human)
                                                                               EST
                                                                                             BF965924.1 GI:12333139
                                                                                                                             mRNA sequence.
                                                                                                                                                             BF965924
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R.Site 2
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'clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="RP43-039L04.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="genomic DNA"
db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Pan troglodytes"
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: EcoRI.
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Pred. No. 1.7e-18;
1; Mismatches 76;
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REFERENCE

AUTHORS

Hominidae; Homo.

1 (bases 1 to 538)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
Venter,J.C.

TITLE

BAC End Sequences

from

Library RPCI-11 for Sequence-Ready

de Jong, P. and

SOURCE

ORGANISM

Homo sapiens (human) Homo sapiens Eukaryota; Metazoa;

Chordata; Craniata; Euarchontoglires; Pi

Primates;

Vertebrata; Euteleostomi;

Catarrhini,

Mammalia; Eutheria;

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                   AQ341973
AQ341973.1
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RPCI11-111D18.TV RPCI-11
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                            genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                        CAGGCGTGGTGGCGCACATCTGTAGTCCCAGCTACTCGGGAG--GCTGAAGCACGAGAAT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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/mol_type="mRNA" | 9606" |
/db xref="taxon:9606" |
/clone="TMAGE:4365117" |
/tissue_type="osteosarcoma, cell line" |
/clone="lib="NIH_MGC 86" |
/clone="lib="NIH_MGC 86" |
/clone="lib="NIH_MGC 1: NotI; site_2: Site_1: NotI; |
/site_2: Sall; Cloned unidirectionally; oligo-dT primed. |
/Average insert size 1.533 kb Library enriched for |
/full-length clones and constructed by Life Technologies. |
/Note: this is a NIH_MGC Library."
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                       GI:4166869
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Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                              AA648957
AA648957.1 GI:2575386
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                              Hominidae; Homo.
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                             repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
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Fax: 301 838 0208
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/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA
/db_xref="GDB:7542329"
/db_xref="taxon:9606"
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/sex="Male"
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Pred. No. 2.1e-18;
1; Mismatches 65
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                                                                                                                                                                                                                    DR759556
DR759556.1
EST.
Hominidae; Homo.
1 (bases 1 to 897)
                                                                                                                                                                                                                                                                                                                      DR759556 897 bp
HESC4_105_B07.gl_A037 NIH_MGC_262
IMAGE:7968807 5', mRNA sequence.
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unknown library type
Seq primer: -40ml3 fwd. ET f
                                                                                                                                            Homo sapiens (human)
                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg,
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                                                                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAAAAAAAAAA 85
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//note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
/note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
/note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
/note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
/note="Vector: ptropy state of the content                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 2.4e-18;
L; Mismatches 82;
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RESULT 17
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 196;
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Plate: LLAM 17081 row: c column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Laboratory for Genomics and Bioinformatics, University of Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: BresaGen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                         TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGGTCAAGAGA 140
                                                 CAAAAAGAAAAAAAAA 848
                                                                                    CAAAAACAACAACAAAAAAC 340
                                                                                                                            CTTGAACCCAGAAGGTGAAGGGCACAGTGACC---
                                                                                                                                                            TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                       TCGAGACCAGCCTGGCCAACATGGTGAAACTCCCATCTACTAAAAATACAGAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer: JENREV (CAGGAAACAGCTATGACC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 897.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library Preparation: Express Genomics, Inc. Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: PExpress-1; Site 1: Not1; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BGO1.
Positive for Nestin and Mussahi expression. Passage number
18. cDNA primed using oligo-dT primer:
18. cDNA primed using oligo-dT primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. this is a Mammalian Gene Collection library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH MGC 259). It was constructed by Express Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="human embryonic stem cells"
/cell_line="BG01"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="embryonic stem"
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db_xref="taxon:9606"
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75.4%;
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Pred. No. 2.
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ches 59;
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PUBMED
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DA500385/c
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Best Local Similarity
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                                                  321 САВАВАСАВСАВСАВВАВАВСАВВВАВАВ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-400-20 Fax: Brail: flj-cdna@nifty.com
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Research Association for Technology and Evaluation; 3'-end
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DA500385.1
EST.
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Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.

(bases 1 to 486).

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, J., Sekine, M., Tsono, Y., Irie, R., Kushida, N., Yamayama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Sigai, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification and Characterization of Putative Alternative Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-438-52-3975
Fax: 81-438-52-3986
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TAAATAAATAAATAAAATACA
                                                                                                                                                              TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                                        TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
/dev_stage="fetal"
/clone_lib="FCBBF3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="FCBBF3014320"
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Pred. No. 2.7e-18;
0; Mismatches 75;
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clone FCBBF3014320
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Best Local Similarity
Matches 192; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
DA180817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pass sequencing: RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takao Isogai
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EST.
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DA180817 BRAMY2 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                       TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                    CAMAMACAACAACAAAAAACAAAAAAA 347
                                                                                                                                                                                                                                                                                                                                        ACGCCTATAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                     TCAAGACCAGCCTGGCCAACACAGTGAAAACCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                              CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA
                                                                                                                                                                  TGGGCATGATGCTGCATGCCTGTAATCCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="amygdala"
/clone_lib="BRAMY2"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAMY2045648"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.8%;
71.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 147; DB 9;
Pred. No. 2.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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cDNA clone BRAMY2045648
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8 5', mRNA
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KEYWORDS
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BG258140/c
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                                                                                                                                                                                                                                                                                   141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                            192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG258140 545 bp mRNA linear EST 13-FEB-2001 602379239F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4510256 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LLAM10391 row: m column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                      CAAAAACAACAACAAAAAAAACAAAAAAA 347
                                                                              CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 206
                                                                                                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                          TCAAGACCAGCCTGGCCAACACAGTGAAACCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
TAAATAAATAAATAAATAAAATACA 179
                                                                                                                                                                                                  TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                           ACGCCTATAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryonal carcinoma, cell line"
/lab host="DHIOB (phage-resistant)"
/clome libe"NIH MGC 92"
/clome libe"NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site 2: SalI; Cloned unidirectionally; Oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4510256"
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71.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 147; DB 2;
Pred. No. 2.7e-18;
0; Mismatches 75
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                                                                                                                                                                                                                                            326
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RESULT 20 DA158439/c

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Best Local Similarity
Matches 192; Conserv
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                                                                                                                                                                                                                                                              312
                                                                                                                                                                                                                                                                                                                                                   372
132
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                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                  141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                         81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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1 (bases 1 to 547)

1 (bases 1 to 547)

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S. Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); CDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DA158439 BRAMY2 Homo sapiens cDNA clone BRAMY2017998 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Takao Isogai
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TAAATAAATAAATAAATAAAATACA 106
                                        CAAAAACAACAACAAAAAAACAAAAAAA 347
                                                                                                                           TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                        TGGGCATGATGCTGCATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
                                                                                                                                                                                                                                                              TCAAGACCAGCCTGGCCAACACAGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                     CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGAACTCCGTCTCCCAAAAAA 133
                                                                                                                                                                                                                 TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="amygdala"
/clone_lib="BRAMY2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAMY2017998"
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147; DB 9;
Pred. No. 2.7e-18;
0; Mismatches 75
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LOCUS
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DB176347
DB176347.1
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DB176347
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.

Murakawa, K., Ishida, S., Ishidashi, T., Takahashi, Tenjii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S

Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bemail: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu,
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Takao Isogai
FLJ Project (HRI Team)
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                                                                                                                                                                                                                                                                                                                                              ACGCCTATAATCCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGAGT 327
                                                                                                                                                                                                                                                                                                                                                                       ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
TAAATAAATAAATAAAATAAAATACA 120
                                     СААЛАЛСЛАСААСЛАЛАЛАСЛАЛАЛАЛ 347
                                                                                  CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 147
                                                                                                                          TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                    TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                            TCAAGACCAGCCTGGCCAACACAGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                  TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TKIDN2012877"
/tissue_type="kidney, tumor
/clone_Tib="TKIDN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pME18SFL3"
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71.9%;
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Pred. No. 2.7e-18;
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7 5', mRNA
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AUTHORS
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1 (bases 1 to 581)

1 (bases 1 to 581)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamocto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Yoneyama, T., Otsuka, R., Ishibashi, T., Takahashi, Thujii, A., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Thujii, A., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Thujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix: Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
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2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
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Genome Res. 16 (1), 55-69
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                        САЛАЛАСАЛСАЛСАЛАЛАЛСАЛАЛАЛА 347
                                                                                            CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 340
                                                                                                                                                                                                                                                                                                                                  TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
TAAATAAATAAATAAAATAAAATACA 313
                                                                                                                                          TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                                                         TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="brain"
/dev_stage="fetal"
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/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="OCBBF3024884"
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Pred. No. 2.7e-18;
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89
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Plate: LLAM12234 row: h column: 14
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AGENCOURT_6436650 NIH_MGC_72 Homo sapiens cDNA clone
5', mRNA sequence.
BM542252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Eukaryota; Metazoa;
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1 (bases 1 to 1085)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                      CAAAAACAACAACAAAAAAACAAAAAA 347
                                                                            CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 90
                                                                                                                                                                                                                                                                                                                             ACGCCTATAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGATCACCTGAGGTCAGGAGT
TAAATAAATAAATAAAATAAAATACA 63
                                                                                                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                             TGGGCATGATGCTGTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
                                                                                                                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                   ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                 TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                            TCAAGACCAGCCTGGCCAACACAGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 147; DB 2;
Pred. No. 2.4e-18;
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MAGE:5539645
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RESULT 24 AQ381551/c LOCUS

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RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                     208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Other GSSs: RPCII1-165E2.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence.
AQ381551
AQ381551.1 GI:4352574
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Venter,J.C.
Use of BAC End Sequences from Library RPCI
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                                                                                                                                                                                                                                                                                                                                                                               CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                                                                                                             -----CCAAGATTGCACCACTGCACTCCAGTCTGGGCGACAGAGTGAGACTCCATCTCAA
                                                                                                                                                                                                                                                    GCATGGTGGCACACCCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="GDB:7563073"
/db_xref="taxon:9506"
/clone="RPCI-11-165E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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71.7%;
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e_lib="RPCI-11"
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Pred. No. 2.9e-18;
*** *** *** ** 73;
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Best Local Similarity
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EST.
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Plate: LLCM2353 row: i column: 04
High quality sequence stop: 555.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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1 (bases 1 to 775)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CAAAAACAACAACAAAAAAACAA 342
                                                                                 TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                                                                                                                                                                     TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                          ACGCCTGTAATCTCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGT
                                        TGGGCATGGTGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3' adaptor sequence:
5' -ATTCTAGAGGCCGAGGGGGGGGGAGATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Pale
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0; Mismatches 72
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crllh09.x1 Human bone marrow
HBMSC:crllh09 3', mRNA sequen.
A1753536
A1753536.1 GI:5131800
EST.
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Gene expression profile of human bone marrow stromal cells: high-throughput expressed sequence tag sequencing analysis genomics 79 (1), 7-17 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 11 row: h column: 09
Seq primer: -21M13 forward primer (ABI).
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10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
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Medical Genetics Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: libin@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                     Similarity
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ATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA
                                                                                                                                                                          CCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCGGAGGTCAGGAGTTCGAGACCAGCC
                                                                                                                                                                                                         CCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCC
                                                CAGGCACCTGTAATCCCAGCTACTAGGGAGGCTTTTGAACCCAGGAGGCAGAGGTTGCAG
                                                                              CACACACCTGTAGTCCCAGCTACTCAGGAG-----CCGGAGATTGCAGTGAGCTGAG
                                                                                                             TTGCCAACATAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGG
                                                                                                                                             TGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGG
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/mol type="mRNA"
/db xref="teaxon:9606"
/clone="HBMSC cr11h09"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Human bone marrow stromal cells" /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI; /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI; mRNA made from human bone marrow stroma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected for average insert size >0.5 kb. Library constructed by Dr. Marian Young and Dr. Pamela Gehron Robey (NIDCR). Library supplied by Dr. Libin Jia (NHGRI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="bone marrow stroma"
/dev_stage="mixed"
/lab_host="XL1-Blue MRF'/SOLR"
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Pred. No. 3.3e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1365 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 490)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria;
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GCTGAGGTAGAAGAATCACTTGAACCCAGGAGGCAGAGGCTCCAGTGAGCCGAGATTACG
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                                         CCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG
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/db xref="taxon:9606"
/clone="IMAGE:2132539"
/tissue_type="lymphoma, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
/clone lib="NCI_CGAP_Lym12"
/clone lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
/note="Cryan: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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Pred. No. 3.3e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-85-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 667)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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/clone="RP43-020P17.T7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Pan troglodytes"
/mol_type="genomic DNA"
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78.2%;
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Matches 162; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 406)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Dias Neto, E., Garcia Correa, R., Zago, M.A., Bordin, S., Costa, F.F.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bala, G.S., Simpson, D.H.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW902341 406 bp mRNA linear QV3-NN1023-130500-179-b08 NN1023 Homo sapiens cDNA, AW902341
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                            TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                                                                                                                                                                                                                       ACGCCTGTGATCCCAGCACTTTCAGAGGCCGAGGCAGGCGGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                                                  ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
CGAGATAG 114
                                              TGAGATCG 268
                                                                                        TGGGCGTGGTGGTGGGCACCTGTAGTCCCAGCTACTCAGGAGGCAGAGGTTGCGGTAAGC
                                                                                                                                  TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
                                                                                                                                                                                TCGAGACCAGCCTGGCCAATATGGTGAAACCCCGTCTCTACTAAAAAATACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Pred. No. 3.7e-18;
0; Mismatches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AI302156.1 GI:3961502
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524 bp mRNA linear EST 03-DEC-1998 qm58a05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1902416 3' similar to contains Alu repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 524)
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GAGCGAGACTCTGTCTCAAAAATAATAATAATAATAATAATAATAAAAA 163
                                                                                                                 TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG------CA
                                   CTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCCGAGACCGTGCCTCCAGCCTGGGTGACA
                                                                                                                                                        TGGGCATGGTGCACACCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTAGGAGAGTGG
                                                                                                                                                                                                                                         TCGAGACCAGCCTGGCCAACATGGTGAAAACCCCGTCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                   quality sequence stop: 461.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Kid5"
/note="Organ: kIdney; Vector: pT7T3D-PacI; Site_1: Not
Site_2: Eco RI; 1st strand cDNA was primed with a Not J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1902416"
/tissue_type="2 pooled tumors (clear cell
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="mRNA"
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Agowa (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project
This clone (DKFZp470B1412) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp470B1412 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR860050
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1 (Dases 1 to 1459)

Wambutt,R., Heubner,D., Mewes,H.W.,
Fobo,G., Han,M. and Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus (orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR860050
                                                                                                                                 TAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGG
                                          AGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGT 165
                                                                                      TAAGAAGCTGGATCTCCTGCCAGGCGCGCGGTGGCTCATGCCTGTAATCCCACCACTTTGGG
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYGmaeus mRNA; cDNA DKFZp470B1412 (from clone DKFZp470B1412).
                                                                                                                                                                                                                                                                                       /translation="mkpilloghersitqikynregdllftvakdpivnvwysvnger
lgtynghtgavwcvdadwpykhvlygsadnsgrlwdcetgkolallkynsavpetgep
rggsiimfestkomgyocfvsffbladbsqidndiolskitsavwgplegec
iiaghesgelnqysaksgevlvnvkehsrqindiolsrdmymfvtaskontaklfdst
tlehoktfrtertervnsaalspnydhvvlgggebamdvtttsyrdigkfearffhlaffee
efgrvkghfglinsvafhpdgksyssggedgyvrihyfdpqyfeffefea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pongo pygmaeus"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="texon:9600"
/clone="DKrZp470B1412"
/tissue type="liver"
/clone lib="470 (synonym: pliv1). Vector pSport1_Sfi; host DH10B; sites SfilA + SfilB"
/dev_stage="adult"
/note="TGF-beta receptor interacting protein 1 (Homo
                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="CAH92198.1"
/db_xref="GI:55730962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15. .992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="DKFZp470B1412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="DKFZp470B1412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:55730961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1459
                                                                                                                                                                                                  36.6%;
                                                                                                                                                                         Score 146.4; DB 6
Pred. No. 2.9e-18;
D; Mismatches 66
                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weil, B.,
                                                                                                                                                                           66;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amid, C.,
                                                                                                                                                                                                                          1459;
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                                                                                                                                                                           0,
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                                                                                                                                                                           Gaps
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166 GAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAG

225

AGGCCAAGGTGGGCGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGACCAACATGGA 1109

밁 á В 5

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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1110 GAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGGCACACGCCTATAG 1169
  119
                                       261
                                                                               179
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                                                                                                                                                                                                       141
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                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brandenberger, R., Wei, H., Zhang, S., Li, Y., Xu, C., Fang, R., Guegler, K., Lebkowski, J and Stanton, L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CN268905 302 bp mRNA linear EST 16-MAY 17000597786250 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 Constitution Drive, Menlo Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Brandenberger
Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CN268905.1 GI:47285319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN268905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGATCACAGA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATC 285
                                                                                                       TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                    TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
CGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGC
                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC
                                                                               CGGGCGTGGTGGCGGCCCTGTAGTCCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGG
                                                                                                                                                               TCAAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCCTTACTACAAATACAAAAATTAGC
                                                                                                                                                                                                                                               ACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTAGGCGGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                       ATGCCTGTAATCCCCAGCACTTCCGGGAGGCCAAGGTGGGCCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGAGCTGAGA 1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 302)
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="GRN_PREHEP"
/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="embryonic stem cells, DMSO-treated H9
                                                                                                                                                                                                                                                                                                                                          36.6%;
78.5%;
                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                            Score 146.2;
Pred. No. 4.3
                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                              4.3e-18;
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                                                                                                                                                                                                                                                                                                                                                               DB 8;
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                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                 Length 302;
                                          303
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                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell
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                                                                                                                                                             180
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299

141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC

ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140 ACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGT

Matches Query Match Best Local

195;

Conservative

Local

Similarity

36.6%; 75.3%;

Score 146.2; DB Pred. No. 4e-18; L; Mismatches

DB 3; 59;

Indels Length

4.

Gaps

240 200

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REFERENCE
AUTHORS
TITLE
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SOURCE
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BM712012/c
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-181, >ALU (matched compliment) 55-316, >ALU (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Iowa
University of Iowa
Joseph Colone Distribution: Research colone Soares, University of Iowa
Olone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 419)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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419 bp mRNA linear EST 28
UI-E-DW1-ahc-a-08-0-UI.r1 UI-E-DW1 Homo sapiens cDNA clone
UI-E-DW1-ahc-a-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8889548
Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
             following tissue(8): Lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an BooR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="U1-E_DH1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
U1-E-DW1 is a normalized cDNA library containing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-DW1-ahc-a-08-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="lens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                >ALU (matched compliment) 55-316, >ALU (matched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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RESULT 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                       Query Match
Best Local Similarity
Matches 157; Conserv
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                           201
                                                         377
                                                                                    141
                                                                                                                 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 Constitution Drive, Menlo Park, Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,Y., Xu,C., Fang,R., Guegler,K., E
Lebkowski,J and Stanton,L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN351916 680 bp
17000532267149 GRN_EB Homo sapiens
CN351916
CN351916.1 GI:47351850
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rbrandenberger@geron.com
Insert Length: 680 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.
1 (bases 1 to 680)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15146197
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               TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAG 255
                                                                        TCGAGACCATCCTGGCCAACATGGTGAAAACCCCGGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                               ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAAGTGGGCAGATCACCTGAGGTCAGGAGT
                                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
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 TGGGCATGGTGGCGCACACCTGTAATCCCAGCTACTCCGAAGGCTGAGGCAGGAG
                                                       TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGC
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                                                                                                                                                                         Conservative,
                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone_lib="GRN_BB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                     36.6%;
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                                                                                                                                                                                  Score 146.2; DB 8
Pred. No. 3.7e-18;
                                                                                                                                                                       Mismatches
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VERSION
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BE379282/c
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             111
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                                       321
                                                                                                  261
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                                                                                                                                                                                                                                                                                                      195;
             CAAAAAGAAAAGAAAAA
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cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LicM265 row: i column: 08
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 4 High quality sequence stop: 634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BE379282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE379282.1 GI:9324647
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                                                                                                    CTTGAACCCAGAAGGTGAAGGGCACAGTGACC---
                                                                                                                                                    TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                               САЛАЛАСЛАСАЛСАЛАЛАЛ 339
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                                                                                                                                                                                                                                                                                                                       TCGAGACCAGCCTGGCCAACATGGTGAAACTCCATCTCTACTAAAAATACAGAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)"
/clone lib="NIH MCC 44"
/clone lib="NIH MCC 44"
/clone lib="NIH MCC 44"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Si
RooRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling H
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
mol_type="mRNA"
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93
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Pred. No. 3.7e-18;
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CN411940/c
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Best Local Similarity
Matches 195; Conserv
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AA836548
323 bp mRNA linear EST 24-FEB-1998 od36h04.51 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1370071 similar to contains Alu repetitive element;contains element PTR5 repetitive element;, mRNA sequence.

AA836548
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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Tel: 650 473 8658
Fax: 650 473 7760
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CN411940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rbrandenberger@geron.com
Insert Length: 805 Std Error:
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Homo sapiens
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                                                                                                                                                                       CAAAAGAAAAAGAAAAA
                                                                                                                                                                                                                                                                                                                        TGGGTATGGTGCATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="embryonic stem cells, cell lines H1, H7, and
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75.3%;
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Pred. No. 3.6
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Best Local Similarity
Matches 206; Conserv
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., I
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa;
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA836548.1
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1 (bases 1 to 323)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                   TCGAGACCATCCTGGCCAACATGGTGAAAACCCCGGTCTTTACTAAAAAATACAAAAAAATAGC
                                CKCCGTCTCAAAAACAACAACAAAAAAACAAA 343
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                                                                                           CTTGAACCCAGAAGGCGGAGGTTGCAGTGAGCCGAGATCAACCTGGGAGACAGAATGAGA
                                                                                                                                          --TGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG-CAGAGTGAGA
                                                                                                                                                                                                                                      TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAG-----
                                                                                                                                                                                                                                                                                        TGGAGACCAGCCTGGCCAACATGGCAAAAACCTGTCTCTACTAAAAATTACAAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="NCI GAAP GCB1"
/clone lib="NCI GAAP GCB1"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
/note-index for germinal center B cells by flow sorting
/enriched for germinal center B cells by flow sorting
/cd20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr.
David Allman (NCI) and Dr. Gerald Marri (CEBR). CDNA
/enriched Synthesis was primed with a Not I - oligo(dT) primer
/enriched Synthesis was primed with a Not I - oligo(dT) primer
/enriched Synthesis was ligated to Eco RI adaptors
/enriched Synthesis was ligated to Eco RI adaptors
/enriched Synthesis was ligated to Loned into the Not I
/enriched Synthesis was ligated to Loned into the Not I
/enriched Synthesis was ligated with Not I and cloned into the Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:1370071"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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1; Mismatches 56
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BQ267427/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq.primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 355.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endocrine Pancreas Consortium 
Unpublished (2000)
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BQ267427
BQ267427.1 GI:20492492
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 416)
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                                          TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                         TCGAGACCAGCCTGACCAATATGATGAAACCCCCGTCTCTA-AAAAAATACAAAAATTAGC
                                                                                                                                      TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                      ACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGGTGGGCAGATCACCTGAGGTCAGGAGT
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  (http://genome.wustl.edu/est/lambda protocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Perm Laboratory, Washington University School of Medicine, 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this a Washington University Pancreas EST project library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: pancreas; Vector: pBluescript SK-, Site_1: XhOI; Site_2: EcoRI; Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5780494"
/tissue_type="insulinoma"
/lab host "DH10B (phage_resistant)"
/clone_lib="Human insulinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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78.0%;
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Pred. No. 5.7e-18;
1; Mismatches 47;
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                                                                                                                                                                                   Best Local Similarity
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141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321
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                                                                      97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seatt
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.

1 (bases 1 to 464)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ598684 1inear GSS 08-JUN 1inear GSS 08-JUN HS_5336_B2_E09_SP6E RPCI-11 Human Male BAC Library Homo sapien genomic clone Plate=912 Col=18 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 464
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.htsc.washington.edu
Plate: 912 row: J column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                                      ATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACCTGAGGTCAGAAGC 156
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                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                              sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="Plate=912 Col=18 Row=J"
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                                                                                                                                                                              36.4%;
72.6%;
                                                                                                                                                                                                                                                                            .6 vector at EcoRI sites"
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                                                                                                                                                      Score 145.4; DB 11;
Pred. No. 5.6e-18;
Wismatches 67;
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Human Male BAC Library Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Leenishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ269776 518 bp mRNA linear EST 15-JUL-2003 ik30a05.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5782185 3' similar to SW:ALU7 HUMAN P39194 ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY. [1]; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing
Washington University Genome Sequencing Center For informati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
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         /lab nost="univ"
/clone lib="HR85 islet"
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: priming."
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~lbb. 5'
XhoI site was destroyed after directional cloning.
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Buclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:5782185"
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DA175472.1
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DA175472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (bases 1 to 551)

1 (bases 1 to 551)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, K., Isono, Y., Irie, R., Kushida, N., Yoheyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M. Murakawa, K., Ishidashi, T., Takahashi, F. Ujii, A., Marakawa, K., Ishidashi, T., Nakahashi, F. and Sugano, S. Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                   Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HR.
Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                           Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Takao Isogai
FLJ Project (HRI Team)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                      Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promoters of Human Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16344560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAAAAAAAAAAGCCAAAAACAAAACAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAAACAACAACAAAAAACCAAAAAACCATAAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGCATAGTGGCAGCCTGTAATCCCAGCTACTCTGGAGGCGGAGGTTGCAGTGAGC
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                                                                                                                                                                                                                                                                                                                                                                81-438-52-398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRAMY2 Homo sapiens
                 /tissue_type="amygdala"
/clone_lib="BRAMY2"
/note="Vector: pME18SFL:
                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                              organism="Homo sapiens
                                                                                  clone="BRAMY2038827"
                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:78720791
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Pred. No. 5.5e-18;
                 PME18SFL3"
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DW412368
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Best Local S
Matches 209
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Best Local Similarity
Matches 191; Conserv
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                                                                                                                                                                                                                                                                                                                       source
                                                            141
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                                                                                                                                                                                                                                                                                                                                                                                                              Henan Bioengineering Key Lab
Henan Normal University
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liver regeneration after Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                   Email: xucs@x263.net.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cun-Shuan Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu,C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DW412368.1 GI:84913924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HHAGE013098 Human liver regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                               TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
                                                                                                         ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGA-----GCCGGAGATTGC
                            TCGAGACCAGCCTGGTCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAACTAGC
                                                                                        TARATARATARATARATARAATACA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGATCGCACAACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCCCAAAAAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                  148 Jianshe Road, Xinxiang City, : 00863733328084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 324)
                                                                                                                                                                                                                                                                                                                                                                   00863733326524
                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mrN,"
/db xref="raxon:9606"
/tissue_type="liver"
/clone_lib="Human liver regeneration after partial
                                                                                                                                                                                                                           nepatectomy"
                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                               36.3%;
71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.4%;
71.5%;
                                                                                                                                                    0
                                                                                                                                               Score 145.2; DB 10
Pred. No. 6.6e-18;
0; Mismatches 78;
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Pred. No. 5.4e-18;
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KEYWORDS
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DB330188/c
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Best Local Similarity
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                         62 CAGGCATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGG 121
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1 (bases 1 to 498)

1 (bases 1 to 498)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Tahii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Tsoo, Y., Irie, R., Wagatsuma, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Tsoo, Y., Irie, R., Wagatsuma, N.,

Yoneyama, T., Wagatsuma, N., Yakai, K., Isogai, T., Wagatsuma, N.,

Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, T., Takahashi, T., and Sugano, S.

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)
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DB330188
DB330188.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takao Isogai
FLJ Project (HRI Team)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helix Research Institute
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CAGGTACTCAGCCATGTGCTGGGCCATGGGGAACCCAAATATTAATAAGACATTGTCAGGC
                                                                                         CATTTTCTCATGCATCTATTGGTCATTTGTACATCTCTTGAGAAATGTCTTAAAAAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGAACCTGGGAGGCAGAGGTTGCAACCATTGCACTCCAGCCTGGGCGACAAGAGCAAG
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                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="pROST2015815"
/tissue_type="prostate"
/clone_Tib="pROST2"
/note="Vector: pME18SFL3"
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                                                                                                                                                                              0,
                                                                                                                                                                           Score 145.2; DB 9;
Pred. No. 6.1e-18;
0; Mismatches 73;
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clone PROSTZ015815
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                                                                                                                                                                                                                      Length 498;
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222
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JOURNAL
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COMMENT
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AUTHORS
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SOURCE
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DA714821/c
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                                   81
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishidashi, T., Takahashi-Tujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Divergification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DA714821
DA714821 NT2RI2 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                    Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); CDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology
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Helix Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Promoters of Human Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAAAATACAAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGA 241
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                                   ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81-438-52-3975
                                                                           Conservative
                                                                                                                                                                           /note="Vector: pME18SFL3; majorly NT2 neuron; mRNA from
NT2 neuronal precursor cells treated 2-weeks mitotic
inhibitor after 5-weeks retinoic acid (RA) induction."
                                                                                                                                                                                                                                                           /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                        clone
                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                   lone="NT2RI2021923"
                                                                                            36.3%;
                                                                                                                                                                                                                                      _lib="NT2RI2"
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sapiens cDNA clone
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                                                                         Pred. No. 6e-
); Mismatches
                                                                                              Score 145.2;
Pred. No. 6e
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5', mRNA
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                                                                           Gaps
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RESULT 45
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ORGANISM
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                                                                                                                                                                                              Query Match
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                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                       144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other GSSs: RPCIII-96D8.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSD
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RPCI11-96D8.TV RPCI-11 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                          AGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGCTGG
                                                                                                 CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGCATGATGCTGCATGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGTTGCAGTGAGC
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                                                                            CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTCAGGAGTTCG
  AGACCAGCCTGGCCAACATGGTGAAACACCATCTCTACTAAAAATACAAAAATTAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens (human)
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC ends.
                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                               /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6;
                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:7536559"
/db_xref="taxon:9606"
/clone="RPCI-11-96D8"
                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .555
                                                                                                                                                                                                                                                                                                                                                                                                                      _type="genomic
                                                                                                                                                                              36.3%;
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                                                                                                                                                         Score 145.2; DB 11,
Pred. No. 5.9e-18;
1; Mismatches 59;
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genomic clone RPCI-11-96D8,
                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                   EcoRI; Site
                                                                                                                                                             Indels
                                                                                                                                                                                              Length
                                                                                                                                                           14;
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                                                                                                                                                             Gaps
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                                                                                315
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TITLE
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                                                                                                                                                                                 Query Match
Best Local S
Matches 162
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                          162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264
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AGENCOURT 11828537 NICHD Rh_Ov1
IWAGE:6913528 5', mRNA sequence.
CB309712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L/cM3154 row: m column: 15
High quality sequence stop: 454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecidae; Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB309712.1 GI:28832422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (rhesus monkey)
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: CLONTECH cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: NCI_CGAP clone distribution information
                                                                                                                ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCGCAG------AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGACTG 309
                                                                                      ATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCAGATCACTTGAGGACAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACKCCGTCTCAAAAACAACAACAAAAAAAAAAAAAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATCACGCCACTGCATTCCAGTCCAGTG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGTGGTGACGCGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGACTCCGTCTCAAAAAAAAAAAAAGTAAGTTAATTAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 591)
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                          /tissue_type="Ovary"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NICHD_Rh_Ov1"
/clone_lib="NICHD_Rh_Ov1"
/note="Organ: ovary; Vector: pDNR-LIB; Site 1: Sfi I;
Site 2: Sfi I; Cloned unidirectionally. Primer: Oligo
Average insert size 1.0-4.0 kb. Tissue primerted from
pre-pubertal, post pubertal sn menopausal monkeys.
Constructed by Clontech. Note: this is a NICHD Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:6913528"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Macaca mulatta"
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                                                                                                                                                                                                  36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _type="mRNA"
                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                            Score 145.2; DB 4;
Pred. No. 5.9e-18;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta cDNA
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KEYWORDS
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DA408951
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Best Local Similarity
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RS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tguritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishidas, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

AL Genome Res. 16 (1), 55-65 (2006)
  393
                                                                                                                                                                     273 CCTGGACAACTCCCTCTATAAGAAATAGAAAATGAGGCCAGGCACATGGCTCATGTC
                                                                                                                                                                                                                                                           195;
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                                                                                                                            98
                                                                                                                                                                                                            26 CATGGGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end opass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Takao Isogai
FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Primates; Cata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                                                                                                            TGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAG 145
                                    ACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGAACCCAG 477
                                                                                 TGTAATCTCAGCACTTCGGGAGGCTGAGGTGAGCAGATCACTTGAGGTCAGGAGTTCGAG
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRTHA3015134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Locat
                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="thalamus"
clone_lib="BRTHA3"
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                                                                                                                                                                                                                                                                              36.3%;
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                                                                                                                                                                                                                                                                                                                                                                 PME18SFL3"
                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                DB 9;
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CZ459725
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Best Local
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                   204 GCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CZ459725 849 bp
MCF748c16TF Human MCF7 breast ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genomex.com
Class: BAC ends.
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Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: svolik@cc.ucsf.edu
This clone is available from Amplicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Volik SV
Colin Collins' lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
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                                                                                                                                                                                                                                      Similarity
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                                                                                             AGACCATCCTGGCCAACATGGTGAAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
                                                                                                                                                                CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCAGAAGGCGGAGGTTGCAGTGAACCGAGATTATGC 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGTGACACACCTGTAATCCCAGCTACTGGGGAGGCTGAGGCAGGAGAATTGCTTGA 512
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                                                                                                                                             CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGCGGATCACCTGAGGTCAGGAGTTCG
GCGTGGTGACGCGCACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comprehensive Cancer Center
Box 0808, San Francisco, CA
415 502 7066
415 502 5665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens (human)
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                        /note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Human MCF7 breast cancer cell line library
(MCF7 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="MCF7_48c16"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="genomic DN/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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                                                                                                                                                                                                                                   Score 145.2; DB 1
Pred. No. 5.5e-18;
                                                                                                                                                                                                                     Mismatches
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RESULT 49
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DA112846
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1 (bases 1 to 550)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Kimura, K., Wakamatsu, A., Sekine, M., Tsuritani, K., Wakaguri, H., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Kushida, N., Ishila, S., Sugiyama, T., Saito, K., Isono, Y., Irle, R., Kushida, N., Yonoyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, Yonoyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, Diversification and Characterization of Putative Alternative Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: flj-cdna@nifty.com
MEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HR:
Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Promoters of Human Genome Res. 16 (1),
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                                                                                                                                                                                                                                                                                       Similarity
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                                                                                       TTTGAGACCAGCCTGGCCAACATGGTGAAACCCCCATCTCTACTAAAAATCACAAAAATTA 369
                                                                                                                           ATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAT-ACAAAAAATA 198
                                                                                                                                                                                                                       ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCA-CCTGAGGTCAAGAG 139
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  GCCAGGCGTGGTGATGCACACCTGTAATCCCAGCTACTCGGGAGGTGGAGGTTGCAGTGA
                                GCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGA 258
                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="BRJ
/note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="cerebellum"
/clone_lib="BRACE3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="BRACE3030866"
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, 55-65 (2006)
                                                                                                                                                                                                                                                                                     Score 145; DB 9;
Pred. No. 6.5e-18;
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Best Local Similarity
Matches 157; Conserv
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1 (bases) to 555)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Kimura, K., Wakaguri, H., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishil, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishidashi, T., Takahashi-Fujii, A., Murakawa, K., Ishida, S., Ishidashi, T., Takahashi-Fujii, A., Murakawa, K., Ishidashi, T., Takahashi-Fujii, A., Diversification of Transcriptional Modulation: Large-scale Diversification of Transcriptional Modulation: Large-scale
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DA198015
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NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
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2-6-7 Kazusa-Kamatari, Kisarazu, Chiba,
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FLJ Project (HRI Team)
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                                                                                                                                                                                                                                                            Conservative
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="BRAWH2000862"
/tissue_type="brain"
/clone lib="BRAWH2"
/note="Vector: pME18SFL3"
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Db 367 CGGGCATGGTGGCGCACACCTGTAATCCCAGCTACTCCGAAGGCTGAGGCAGGAGAG 311

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| EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
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RESULT 1
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

IITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/21,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
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nes 201; Conservative
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                                  136 AGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAA
                                                                                                                  201;
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GCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCA 135

Score 158.4; DB Pred. No. 9e-37; 0; Mismatches

DB 3;

Length 10980; Indels

71;

0; Gaps

0

GGAGTTTGAGATCAGTCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAATATACAAAAA

4702 195 4762

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-03
1 PRIOR FILING DATE: 2000-10-03
1 PRIOR APPLICATION NUMBER: 60/231,498
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PRIOR FILING DATE: 2000-10-03
1 PRIOR APPLICATION NUMBER: 60/231,498
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; LENGTH: 10980
; TYPE: DNA
; ORGANISM: Human
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; ORGANISM: Human
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: RastSEQ for Windows Version
SEQ ID NO 192208
LENGTH: 601
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Patent No. 681233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGCATGGTGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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Pred. No. 1.2e-37;
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RESULT 3
US-09-949-016-12783/c
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US-09-949-016-17230
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                      Sequence 17230, Apparent No. 681233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12783
LENGTH: 15564
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Matches 201; Conservative
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                                                                                                                                                   Patent No.
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                  GGAAAAAAAAAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                       ССТСТСАВАВАСАВСАВСАВАВАВСАВАВАВА 347
                                                                                                                                                                                                                                                                                                                                                                                           TGAGCCGAAACTGCACCACTACACTCCAGCCTGGGTGACAGAGGGGAGACTCTGTCTCCCA 9175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAGCTGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAG 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAAAAAAAAAAAAAAAAAAAAAAAAA 4550
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                                                                                                                                                        Application US/09949016
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Pred. No. 1e-
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1e-36;
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OF DETECTION AND USES
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RESULT 5
US-09-949-016-13909
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
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                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                      Sequence 13909,
                                                                                                                                                                                                                                                                   Patent No. 681233
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Best Local
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGATCGCAG-----AGTGAGCCGAAATCACAGATCACAGAGTGAGCAGA 306
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                                                                                                                                                                                                                                                                                        Application US/09949016
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75.0%;
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Pred. No. 2.1e-36;
1; Mismatches 57;
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밁 Ś ; ORGANISM: Human US-09-949-016-13909 SOFTWARE: FastSEQ SEQ ID NO 13909 Query Match Best Local Similarity NUMBER OF SEQ ID NOS: 207012 ENGTH: 44789 14253 DNA 200; 18 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140 ATGCCTGTAATCCTGGCACTTTGGGAGGCCAAGGCGTGTGGATCATTTGCGGTCAGGAGT 14312 38.6%; Version Score 154.4; DB 3; Pred. No. 2.4e-35; 0; Mismatches 76; DB 3; Length 44789; 0 Gaps

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US-09-949-016-17302/c

Sequence 17302, Application US/09949016

Patent No. 6812339

; GENERAL INFORMATION:
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US-09-949-016-12542/c
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LENGTH: 173787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/21,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
-09-949-016-12542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6812339
    APPLICANT: VENTER, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Sim hes 203;
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Craig et al.
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Pred. No. 4.2e-35;
1; Mismatches 52
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OF DETECTION AND USES THEREOF
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Best Local
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
NUMBER OF SEQ ID NOS: 207012
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CAAGAAAAAAAAAAAAAAAGCCAA 18118
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                         TGGGCGTGGTGGCGGGACCTGTAATCCCAGCTACTCCAGAGGCTGAGGCTGCAGTGAGC 18194
                                                                                                                                                                                                                                                  TGGÁGACCAGCCTGGCCÁACATGGTGÁAÁACCTGGTCTCTACCAAAAATTACAAAAATTAGC 1825
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Pred. No. 4.2e-35;
1; Mismatches 52;
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; NAME/KEY: misc_feature; LCATION: (1)...(71574); CTHER INFORMATION: n = A,T,C US-09-949-016-15580 US-09-949-016-15580/c ; Sequence 15580, Application US/09949016 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS SOFTWARE: FastSEQ SEQ ID NO 15580 Sequence 15580, Ap Patent No. 6812339 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08 FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14 NUMBER OF SEQ ID NOS: 207012 ORGANISM: Human TYPE: DNA FEATURE: ENGTH: 71574 for Windows Version ASSOCIATED
OF DETECTION AND USES THEREOF

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RESULT 9
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Best Local Similarity 69.8%;
Matches 224; Conservative
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LENGTH: 152524
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GENERAL INFORMATION:
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Matches 198; Conserv
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ORGANISM: Human
-09-949-016-12683
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR ETLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRRESEQ for Windows Version
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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23608 CGAAAGTTGCAGTGAGCCGAGGTCGTGCCACTGCGACAGAGCAAGACTCTGTCTCAAAAA 23549
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                                                                                                                                                                                                                                                                  GCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCCTGG
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                                     AGCCGAAATCACAGATCACAGAGTGAG-----CAGAGTGAGACKCCGTCTCAAAAA 326
                                                                             ATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGAAGAATGGCTTGAACCCGGGAGG
                                                                                                                     ACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTG
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72.8%;
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Pred. No. 5.1e-35;
0; Mismatches 74;
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RESULT 11
US-09-949-016-16011/c
; Sequence 16011, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS (
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/2949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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nes 224; Conserv
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23548
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                                   СААСААСААААААСАААААА 347
                                                                            CGAAAGTTGCAGTGAGCCGAGGTCGTGCCACTGCGACAGAGCAAGACTCTGTCTCAAAAA
                                                                                                                                                           ATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGAAGAATGGCTTGAACCCCGGGAGG
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CAACAACAACAACAACAACAA 23528
                                                                                                                    AGCCGAAATCACAGATCACAGAGTGAG-----
                                                                                                                                                                                  ACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTG
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Pred. No. 7.9e-35;
1; Mismatches 87;
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US-09-949-016-69587/c
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APPLICANT: VENTER, J: Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 16011
LENGTH: 40091
                                                                                                                                                                                                                                                                        SEQ ID NO 69587
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 69587, Appearent No. 6812339
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Matches 219; Conserv
                                                                                                                                                 Matches
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                                                                                                                                                                                 Query Match
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
-09-949-016-69587
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                               Local Similarity 74.(
les 225; Conservative
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                                                                       ACGCCTGTAATCCCAGCACTTTGGGAGGCTAAGGTGGGCCGATCACCTGAGGTCAGGAGT
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                                                                                                         ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA
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     TCGAGACCAGCCTGGCCAACATGGTGAAAACCCTGTCTCTACTAAAAATACAAAAATTAGC
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                                                                                                                                            Score 152; DB 3; L
Pred. No. 2.2e-35;
2; Mismatches 57;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for
SEQ ID NO 12784
LENGTH: 17050
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Matches 201;
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                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(17050)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
11706
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                                 CAAAAACAACAACAAAAAAAAAA 343
                                                                     AGAGATCGTGCCATTGCACTCCAGTCTGGGCGA-----
                                                                                                                                                                  TGGGCATGGTGGCACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                   TCGAGACCAGCCTGGCCAACATGGTGAAACTCCGTCTCTACTAAAAATACAAAAATTAGC
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Pred. No. 1.3e-34;
1; Mismatches 52;
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OF DETECTION AND
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLIC
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US-09-949-016-13784
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13784, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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NAME/KEY: misc feature
LOCATION: (1) ... (17050)

OTHER INFORMATION: n = A,T,C or
-09-949-016-13680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 
EQ ID NO 13680 
LENGTH: 17050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAAAAAAAAAAAAAAAAAAA 11684
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ilarity 76.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
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; LENGTH: 19566
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12096
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION UNMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12096, Ap
Patent No. 6812339
                                                                                                                                 Matches
                                                                                                                                                 Best Local
                                                                                                                                                                Query Match
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ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(20099)
OTHER INFORMATION: n = A,T,C
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196; Conservative
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                                                           AGCAGAGTGAGACKCCGTCTCAAAAACAACAACAAAAAAACAAAAAAACCATAAGACATTG
                                                                                             ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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72.1%;
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                                                                                                                              Score 150.4; DB 3;
Pred. No. 2.7e-34;
0; Mismatches 76;
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Pred. No. 2.1e-34;
l; Mismatches 58;
                                                                                                                                 Indels
                                                                                                                                                                  Length 19566;
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Sequence 14157, Application U.
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: UENTER, J. Craig
TITLE OF INVENTION: WITH HUI
TITLE OF INVENTION: WITH HUI
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US-09-949-016-14114/c
                                                                                                                                                US-09-949-016-14157
                                                                                                                                                                        RESULT 18
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Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION.
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Human
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J. Craig et al.
POLYMORPHISMS IN KNOWN GENES
WITH HUMAN DISEASE, METHODS
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                                                                                                                     US/09949016
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       ASSOCIATED
OF DETECTION AND USES THEREOF
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                                                                                                                                    SOFTWARE: FastSEQ
SEQ ID NO 11940
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11940, Apparent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOUISO?
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                          NUMBER OF
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LOCATION: (1)...(45572
OTHER INFORMATION: n =
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NAME/KEY: misc_feature
LOCATION: (1)...(481115)
OTHER INFORMATION: n = A,T,C
                                                       TYPE: DNA
ORGANISM: Human
FEATURE:
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73.5%;
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US-09-949-016-16723/c
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LENGTH: 157822
TYPE: DNA
ORGANISM: Human
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Best Local Similarity
Matches 205; Conserv
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CLO01307
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version
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CAAAAACAACAACAAAAAAAAAAAAAACCATAAGACA 357
                                         TGAGATTGCACCACTGCTCTTTAGCCTGGGTGA----
                                                                                                                                     CAGGCATAGTGGCAGGCACCTGTAATCCCAGCTACTCTGGAGGCGGAGGTTGCAGTGAGC
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73.5%;
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Pred. No. 1.2e-33;
1; Mismatches 62;
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                   37.3%;
sest Local Similarity 68.4%;
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(22889
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
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KCCGTCTCAAAAACAACAACAAAAAAACAAAAAACCATAAGACAT
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                                                                                                           AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGAC
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Pred. No. 1.9e-33;
1; Mismatches 76;
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OF DETECTION AND
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RESULT 22
US-09-949-016-12517/c
US-09-949-016-12517, Application US/09949016
; Sequence 12517, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

ASSOCIATED OF DETECTION AND

USES

THEREOF

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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 16021
LENGTH: 77994
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US-09-949-016-16021/c
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; ORGANISM: Human
US-09-949-016-16021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
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09-949-016-12517
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                                                                                                              Local Similarity
mes 192; Conserv
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144 AGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
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192; Conserv
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                                     CCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGATTCACTTGAGGTCAGGAGTTCG
                                                                        CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
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72.7%;
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                                                                                                          Score 148.8; DB 3;
Pred. No. 1.4e-33;
0; Mismatches 72;
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RESULT 25
US-09-949-016-13461/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 13460
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Best Local Similarity
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-09-949-016-13460
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
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                                                                      GTCTCAAAAAAAAAAAAAAAAAAAAA 6382
                                                                                                                                          TGAACCCAGGAGGCAGAGGTTGCAGTGAGCACTCCAACCTGGGCAACAGAGTGAGACTCT 6409
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OF DETECTION AND
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

Sequence 13461, Application US/09949016 Patent No. 6812339

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FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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US-09-949-016-152016
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Best Local S
Matches 200
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 152016
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Patent No. 6812339
                                                                         Matches
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Best Local !
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ORGANISM: Human
-09-949-016-152016
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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ORGANISM: Human
-09-949-016-13461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                             LENGTH: 601
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84 CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG
                                                                      213; Conservative
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                                                               Score 148; DB 3;
Pred. No. 3.4e-34;
1; Mismatches 61
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Pred. No. 6.4e-34;
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RESULT 28
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Sequence 2954, Application US/09949002

Sequence 2954, Application US/09949002

Patent No. 6900016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, M
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR PILING DATE: 2000-09-08
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les 176; Conserv
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Pred. No. 3.9e-34;
0; Mismatches 47
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METHODS OF DETECTION

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US-09-949-002-4465/c
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
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TYPE: DNA
ORGANISM: Human
0-09-949-002-2954
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LENGTH: 601
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Best Local
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Patent No. 6900016
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOPTWARE: FastSEQ for Windows Version
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
09-949-002-4465
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                                                                     TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
                                                                                                                                              TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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Pred. No. 3.9e-34;
0; Mismatches 47
                                                                                                                                                                                                                                              Score 147.8; DB 3
Pred. No. 3.9e-34;
0; Mismatches 47
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RESULT 30
US-09-949-002-4466/c
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4466
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Query Match
Best Local Similarity
Matches 176; Conser
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Patent No. 690001
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Best Local
                                                                                                                                            SEQ ID NO 650
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, NOTITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CLO00790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
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CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/231,401
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                      LENGTH: 60
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                                                                                          ORGANISM: Human
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       Conservative
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78.9%;
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     Score 147.8; DB 3;
Pred. No. 2.5e-33;
0; Mismatches 47;
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Pred. No. 3.
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                                       Length 60595;
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ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140

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PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
ELENGTH: 60595
TYPE: DNA
ORGANISM: Human
US-09-949-002-706
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Sequence 13849, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
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Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
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78.9%;
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2.5e-33;
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                                                                           US-09-949-016-13850
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US-09-949-016-13850
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; LOCATION: (1)...(86945)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13849
                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13849
LENGTH: 86945
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: BOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-08
PRIOR FILING DATE: 2000-9-08
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n =
                                                                                                                                                       FEATURE:
                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                        TYPE: DNA
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73.5%;
                 37.0%;
73.5%;
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Pred. No. 2.9e
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RESULT 35
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n = A,T,C or
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    GAGTGAGACKCCGTCTCAAAAACAACAACAAAAAACAAAAAA
                                               CTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCATTGTACTCCAGCCTGGGCAACA
                                                                                         TGAGATCGCAGAGTGAGCCGAAATCACAGAT-----
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73.5%;
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Pred. No. 2.9e-33;
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; OTHER INFORMATION: n = A,T,C
US-09-949-016-13852
RESULT 37
US-09-949-016-13853
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 13852
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Best Local Similarity
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NAME/KEY: misc_feature
(1)...(86945)
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                                                                                                                           GAGTGAGACKCCGTCTCAAAAACAACAACAAAAAAACAAAAAAA 347
                                                                                                                                                                       CTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCATTGTACTCCAGCCTGGGCAACA 25242
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: U\$/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

ASSOCIATED OF DETECTI

DETECTION AND USES THEREOF

Sequence 13853, Application US/09949016 Patent No. 6812339

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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION A
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US/99/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIO
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U$-09-949-016-13854
                                                                                                                           Query Match
Best Local S
Matches 208
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Patent No. 6812339
GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1383
LENGTH: 86945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 13854
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 86945
TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                         -09-949-016-13854
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                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n = A,T,C or
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LOCATION: (1)...(86945)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                           Local Similarity
nes 208; Conserv
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                                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                                                                                              Conservative
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pred. No. 2.9e-33;
1; Mismatches 58;
                                                                                                                       Score 147.8; DB 3
Pred. No. 2.9e-33;
1; Mismatches 58
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                                                                                                                       58;
                                                                                                                       Indels
                                                                                                                                                                                      Length 86945;
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25062
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; OTHER INFORMATION: n = A,T,C
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US-09-949-016-13855
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR TILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 208; Conserv
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LENGTH: 86945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(86945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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25243
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                               GAGTGAGACKCCGTCTCAAAAACAACAACAAAAAAAACAAAAAAA 347
                                                                  CTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCCATTGTACTCCAGCCTGGGCAACA
                                                                                                 TGAGATCGCAGAGTGAGCCGAAATCACAGAT-----
                                                                                                                                        TGGGCGTGGTGCTGCCCTATAATCCTAGCTACTCAGGAGGCTGAGGTTGCAGTGAAC
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                                                                                                                                                                                                                                                                                                                                                Score 147.8; DB 3
Pred. No. 2.9e-33;
1; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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; LOCATION: (1)...(86945)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-13856
                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                     PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Best Local Similarity
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows SEQ ID NO 13857
                                                                                                                                                                                                                                                                                                                                     Sequence 13857, Application US/09949016
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ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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73.5%;
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Pred. No. 2.9e-33;
1; Mismatches 58
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OF DETECTION AND
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; NAME/KEY: misc feature
; LOCATION: (1)...(86945)
; OTHER INFORMATION: n =
US-09-949-016-13857
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US-09-949-016-13858
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Best Local Similarity
Matches 208; Conserv
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SEQ ID NO 13858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13858, Application US/09949016
                                                                                                                          Matches 208;
                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                            ORGANISM: Human
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(86945)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                       LENGTH: 86945
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TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAAATACAAAAAATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAATAGC 200
                                                      ATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATTACTTGAGGTCAGGAGT
                                                                            ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                          for Windows Version
                                                                                                                                     37.0%;
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Pred. No. 2.5
                                                                                                                          Score 147.8; DB 3
Pred. No. 2.9e-33;
L; Mismatches 58
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                                                                                                                                                            Length
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                               RESULT 44
US-09-949-016-12819
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U$-09-949-016-14022
                                                                APPLICANT: VENTER, J.
                                                                                                                Sequence 12819, Ap
Patent No. 6812339
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Best Local (
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LENGTH: 9798
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ORGANISM: Human
-09-949-016-14022
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE; CL001307
                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                              1195
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                                                                                                                                                                                                                                                                                                           AAACAACAACAAAAAACAAAAAA 347
                                                                                                                                                                                                                                                                                                                                                          GATCACAGCCCTGCACTCCAGCCTGGGTGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACGAAAAACAAAAAACAGCACAA 1218
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                                                                                                                                         Application US/09949016
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J. Craig et al.
POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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75.4%;
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Pred. No. 1.4e-33;
1; Mismatches 55;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 12819
                                                                                                                                                                                                                                                                                                                                                                                           Matches 199;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                         1144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version
                                                                         GATCACAGCCCTGCACTCCAGCCTGGGTGA---
                                                                                                                                                       ACATGGTGGCACGTGTAATCCCAGGTACTCAAGAGGTGGAGGTTGCAGTGAGCGGA
                                                                                                                                                                                           GCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGA
                                                                                                                                                                                                                                                                                                                CCTGTAATCCCGGCACTTTGGGAAGCCAAGGCAAGGCAGGTTGCTTGAGGCCAGGAGTTCA
AACGAAAAACAAAAAACAGCACAA 1218
                                  АЛАСААСААСАЛАЛААСАЛАЛАЛА 347
                                                                                                                GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA
                                                                                                                                                                                                                                                                         AGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAATAGCTGG
                                                                                                                                                                                                                                                                                                                                                    CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              36.9%;
75.4%;
                                                                                                                                                                                                                                                                                                                                                                                         Score 147.6; DB 3
Pred. No. 1.4e-33;
1; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                           CAGAGCGAGACTCCATCTCAA 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9801;
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                323
                                                                                                                                                       1143
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US-09-936-271C-56
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US-09-936-271C-56
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/936,271C
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/CA00/00258
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/124,260
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/127,386
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: US 60/144,919
PRIOR APPLICATION NUMBER: US 60/144,919
                                                                       SEQ ID NO 56
LENGTH: 11820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/09936271C Patent No. 7022497
                                                                                                                              NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yousef, George M.
APPLICANT: Diamandis, Eleftherios
TITLE OF INVENTION: No. 7022497el 1
                                                                                                                                                                                    PRIOR FILING DATE: 1999-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: MTS3USA
                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7022497el Human Kallikrein-Like Genes
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Best Local Similarity Matches 199; Conserv

Conservative

36.9%;

Score 147.6; DB Pred. No. 1.5e-33 1; Mismatches 5

DB 5;

Length 11820; Indels

9;

Gaps

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Query Match

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; LENGTH: 26967
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR FILING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR FILING DATE: 2000-09-08
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US-09-949-016-12926/c
RESULT 47
US-09-949-016-15831/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VENTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 12926, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO 12926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATGGTGGCACGTGCCTGTAATCCCAGGTACTCAAGAGGTGGAGGTTGCAGTGAGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    АВАСВАСВАСВАВАВАСВАВАВА 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCACAGCCCTGCACTCCAGCCTGGGTGA------CAGAGCGAGACTCCATCTCAA 2936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCG 143
                                                                                                               CTTGAACCCAGGAGGTGGAGCTGCAGTGAGCCGAGATCATGCCACTGCACTCCAGCCTG 1696:
                                                                                                                                                                                                                                                                             TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGA-----
                                                                                                                                                                                                                                                                                                                                                                                     TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAGACCAGCCTGGGAAACATGGTGAAACCCCCATCTCTACTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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                                                                                                                                                                                                                                                                                                                                    TGGGCGTGGTGGCGCGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGTAGGAGCATCA 1702:
                                                                                                                                                                - GTGAGCAGAGTGAGACKCCGTCTCAAAAAACAACAACAAAAAAACAAAAAAAACCATAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147.4; DB 3;
Pred. No. 2.4e-33;
1; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSOCIATED OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 26967;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-15831
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16792
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 48
US-09-949-016-16792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ
SEQ ID NO 15831
LENGTH: 35104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 16792
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16792, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                            LENGTH: 55114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGAACTGGGGAGGTGACGGTTGCAGTGAGCAGAGACTGCGCCACTGCACACCGGCCTG 4408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAACAGAGCAAGACAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGCATGGTGGCACGTGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCG 4468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 2.6e
0; Mismatches
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER:

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-41,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 49
US-09-949-016-17565
                                                                                                                                                                                                                                                                                                   Query Match | Rest Local Similarity 73.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
-09-949-016-17565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 116955
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CTTGAACCCAGGAGGTGGAGGGGAGCCGAGATCAGCCCGGACAACAGAGCGAGACTCCATC
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                                     TGAGATCGCAGAGTGAGCCGAAATCACAGATCA-CAGAGTGAGCAGAGTGAGACKCCGTC
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                                                                               TGGGTGTGGTGCACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAACTG
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13969
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13969, A Patent No. 681233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF
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AGACKCCGTCTCAAAAACAACAACAAAAAACAAAAAAACCATAAGACA
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 Sequence 270, App Sequence 117314, Sequence 63395, Sequence 117714, Sequence 9771, A Sequence 98771, A Sequence 98771, A Sequence 98771, A Sequence 53278, Sequence 53278, Sequence 53278, Sequence 639460, Sequence 639460, Sequence 13274, App Sequence 13274, App Sequence 14674, App Sequence 760176, Sequence 2392, App Sequence 45529, App Sequence 45529, App Sequence 760176, Sequence 2392, App Sequence 93, Appl Sequence 94, Appl Sequence 100019, Sequence 97, App Sequence 100019, Sequence 15605, App Sequence 15605, App Sequence 15606, A Sequence 15606
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RESULT 1
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Sequence 5648, Application US/10741601
publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPH
TITLE OF INVENTION: STENOSIS, METHOD
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Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
STENOSIS, METHODS OF DETECTION AND USES THEREOF
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US-09-925-065A-741359
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Sequence 11, Appl
Sequence 4, Appli
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Sequence 742, App
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Sequence 753551,
Sequence 49, Appl
Sequence 442, App
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Sequence 98, Appl
Sequence 4513, Ap
Sequence 229704,
Sequence 634598,
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RESULT 2
US-10-741-600-17657/c
; Sequence 17657, Application US/10741600
; Publication No. US20050026169A1
                                         ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(36805)
; OTHER INFORMATION: n = A,T,C
US-10-741-600-17657
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEO ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17657
LENGTH: 3605
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CURRENT APPLICATION NUMBER: US/10/741,
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5648
LENGTH: 36805
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LOCATION: (1)...(36805)
OTHER INFORMATION: n =
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Pred. No. 2.2e-111;
2; Mismatches 1;
Score 397.2; DB 9;
Pred. No. 2.2e-111;
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Best Local Similarity

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RESULT 3
US-10-741-601-5649/c
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Best Local Simi
Matches 397;
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT PILLNG DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FRACTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5649
LENGTH: 75729
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1) ... (75729)
OTHER INFORMATION: n = A,T,C or
10-741-601-5649
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Publication No. US20040166519A1
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ORGANISM: Homo sapiens
FEATURE:
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                           CTAAAAATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGG
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RESULT 5
US-10-741-601-13924/c
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; LOCATION: (1)...(75729)
; OTHER INFORMATION: n =
US-10-741-600-17658
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US-10-741-600-17658/c
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CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17658
LENGTH: 75729
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHIS
TITLE OF INVENTION: MYOCARDIAL INFARCT
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ORGANISM: Homo sapiens
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GENETIC POLYMORPHISMS ASSOCIATED WITH
MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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Gaps

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59003

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CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14097
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-601-14097
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US-10-741-601-14097/c
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT TILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FRStSEQ for Windows Version 4.0
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LENGTH: 201
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Publication No. US20040166519A1
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: STENOSIS, METHODS OF
FILE REFERENCE: CL001500
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TGGTGGCACACACCTGTAGTC 227
                                 CCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCA
                                                      CCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCA 206
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Pred. No. 5.9e-51;
1; Mismatches 1
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Pred. No. 5.9e-51;
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DETECTION AND USES THEREOF
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US-10-741-600-35944/c
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 35944

LENGTH: 201
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CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
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NUMBER OF SEQ ID NOS: 73997
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                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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GENETIC POLYMORPHISMS ASSOCIATED WITH
MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES
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Pred. No. 5.9e-51;
                                                                                                                          Score 199; DB 9;
Pred. No. 5.9e-51;
l; Mismatches 1
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RESULT 9
US-10-741-601-13993/c
Sequence 13993, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: STENOSIS, METHODS OF DET
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13993
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
PILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14660
   Query Match
Best Local Similarity
Matches 196; Conserv
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Publication No. US20040166519A1
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Best Local Similarity
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                                                                       TYPE: DNA
ORGANISM: Homo sapiens
-10-741-601-14060
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ORGANISM: Homo sapiens
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Pred. No. 2.1e
2; Mismatches
Score 197.2; DB 8;
Pred. No. 2.1e-50;
2; Mismatches 0;
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                                 Length
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Sequence 3604, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECT

PILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: MYOCARDIAL INFARCTION,
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 36017
LENGTH: 201
TYPE: DNA
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US-10-741-600-36084/c
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Matches 196;
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Pred. No. 2.1e-50;
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RESULT 13

US-10-741-601-13992/c

Sequence 13992, Application US/10741601

Publication No. US20040166519A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:

TITLE OF INVENTION: STENOSIS, METHODS OF DET

FILE REFERENCE: CLO01500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13992
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US-10-741-601-14059/c
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      Sequence 14059, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: STENOSIS, METHODS
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Best Local Similarity
Matches 196; Conserva
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Best Local :
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TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
STENOSIS, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 1.3e-46;
0; Mismatches 1
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Pred. No. 2.1e-50;
2; Mismatches 0
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; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14559
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-14059
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Sequence 36016, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36016
LENGTH: 201
TYPE: DNA
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ORGANISM: Homo sapiens
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Pred. No. 1.3e-46;
0; Mismatches 1
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Pred. No. 1.3e-46;
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Best Local S
Matches 201
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6505
LENGTH: 16163.
TYPE: DNA
ORGANISM: Homo sapiens
9-09-764-891-6505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6505, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING.DATE: 2003-12-22
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Best Local Similarity
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ORGANISM: Homo sapiens
-10-741-600-36083
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SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 201
                                                                                                                                                                                                                                              Local Sim:
                                                                                                                     136 AGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAA 195
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                                  ATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAG 255
                                                                                                                                                              GGTTCACGCCTGTAATCCCAGCACTCTGGGAGGCCGAGGCGGGTGGATCACCTGATGTCA
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CCAGCTGGGTGGTGGTACACGCTTGTAATCCCAGCTACTCTGGAGGCGGAGGTTGCAG
                                                                                GGAGTTTGAGATCAGTCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAATATACAAAAA
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Pred. No. 1.2e-37;
0; Mismatches 71;
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RESULT 19
US-09-997-722-16
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; LENGTH: 16163
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-414-270
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US-10-091-414-270
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Publication No. US20030224461A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PALIGC1
CURRENT APPLICATION NUMBER: US/10/091,414
CURRENT FILING DATE: 2002-03-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 39.6%;
Local Similarity 73.9%;
                                                                            8412 GGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8443
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                                                                                                               CGTCTCAAAAACAACAACAAAAAAAAAAA 347
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Pred. No. 1.2e-37;
0; Mismatches 71;
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RESULT 19
US-09-997-722-16
; Sequence 16, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: MORTIS, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR FILE REFERENCE: A-71171/RNS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentin version 3.1
; SCG ID NO 16
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; | ORGANISM: Homo sapien
US-10-301-480-603905
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 603905
LENGTH: 997
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Best Local Similarity
Matches 216; Conserv
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Best Local Similarity
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CAAAAACAACAACAAAAAAACA 341
                                                       TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT
                                                                                                 TGGGCATGGTGGCAGGGCCTGTAATCCCAGCTACTCAGGAGGCGGAGGTTGCAGTGAGC
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78.5%;
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75.0%;
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Pred. No. 4.7e-38;
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TYPE: DNA

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ORGANISM: Homo sapien

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APPLICANT: Wand, David G.
TITLE OF INVENTION: Identifiction and Mapping of
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226618
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 577516
                                                                                                                                                                                                                                                                                   RESULT 22
US-10-301-480-577516
US-10-301-480-577516, Application US/10301480
; Sequence 577516, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
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US-10-301-480-1217314/c
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Best Local Similarity
Matches 205; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 1217314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1217314, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/301,480 CURRENT FILING DATE: -2002-11-21 PRIOR APPLICATION NUMBER: US 10/215,598 PRIOR FILING DATE: 2002-08-09 PRIOR APPLICATION NUMBER: US 60/311,695 PRIOR FILING DATE: 2001-08-10 PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 108827.137
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Pred. No. 4.7e-38;
0; Mismatches 48
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US-10-301-480-1190925
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Best Local S
Matches 206
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ORGANISM: Homo mapien
-10-301-480-1190925
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PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
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CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
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                                       CARAACAACAACAAAAAACAAAAAA 347
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                                                                                                                         TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
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Pred. No. 6.9e-38;
1; Mismatches 52
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Pred. No. 6.9
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RESULT 25
US-10-027-632-98771/c
Sequence 98771, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nuc.
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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; ORGANISM: Human
US-10-027-632-98771
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US-10-027-632-98771/c
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APPLICANT: Wang, David G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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CURRENT FILING DATE: 2002-04-30
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hes 217;
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  232
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CAACAACAATAACAAAAAAAAAAACAAGTGCAAGGTCTTGCCTTTGAGTTGGGGTCAGA
                                   CGAGACCACGCCTTTGCACTCCAGCCTGGGCGA-----CAGAGCGAGACTCTGTCT
                                                                                                              TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCT 320
                                                                                                                                                                                                 TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC 260
                                                                                                                                                                                                                                        TCGAGACCAGCCTGGCCAAAATGGTGAAACCCCCGTCTCTACTAAAAATACAAAATTAGC
                                                                                                                                                                                                                                                                              TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                     ACGCCTATAATCCCAGCACTTTGGAAGGCCAAGGTGGGCGGATCACTTGAGGCCAGGAAT 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 155.4; DB 6; Pred. No. 4.5e-37;
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174
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; LENGTH: 1963
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-98771
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US-10-087-192-760/c
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Query Match
Best Local Similarity
Matches 217; Conserv
                                                                                                                  SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 760
LENGTH: 31898
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Best Local
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                                                                                                                                                                                                                                                                            APPLICANT: MOTTIS, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
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CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
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                                                                     ORGANISM: Homo sapiens
10-087-192-760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/198,676 FILING DATE: 2000-04-20 APPLICATION NUMBER: US 60/193,483
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      Conservative
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72.6%;
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Pred. No. 4.5e-37;
1; Mismatches 72
     Score 155.4; DB 6;
Pred. No. 1.4e-36;
1; Mismatches 72;
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RESULT 27
US-09-925-065A-532789/c
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 532789, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo
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AACCCCATCTCTACTAAAAATACAAAATTAGCTGGATGTTGTGGCAGGTGCCTGTAATC
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                                                      CCAGCTACTCAGGAGGCTGAGGCAGGAGAATCTCTTGAACCTGGGAGGCGGAGGTTGCAC
                                                                                       CCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCAC
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Pred. No. 4.3e-37;
2; Mismatches 89
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RESULT 29
US-10-301-480-609460/c
US-10-301-480-609460, Application US/10301480
; Sequence 609460, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
    TITLE OF INVENTION: In the Human Genome
; FILE REFERENCE: 108827.137
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PRIOR FILLING DATE: 2000-11-20
PRIOR PELLOATION NUMBER: US 60/250,092
PRIOR PELLOATION NUMBER: US 60/250,092
PRIOR PELLOATION NUMBER: US 60/261,766
PRIOR PELLOATION NUMBER: US 60/289,846
PRIOR PELLOATION NUMBER: US 60/289,846
PRIOR PILLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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ORGANISM: Homo sapiens
-09-925-065A-532789
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24
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Pred. No. 4.3e-37;
2; Mismatches 89
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                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1222869
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US-10-301-480-1222869/c
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US-10-301-480-609460
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FREESEQ for Windows Version 4
SEQ ID NO 1222869
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT FILING NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
                                                                      Matches
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1222869, Application US/10301480 Publication No. US20060057564A1
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 609460
LENGTH: 977
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                                                                  Score 153.6; DB:
Pred. No. 1.2e-36,
1; Mismatches 90
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Pred. No. 1.2e-36;
1; Mismatches 90;
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US-10-995-561-13274/c
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1):..(415117)
OTHER INFORMATION: n = A,T,C o
US-10-995-561-13274
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13274
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Publication No. US20050272054A1
GENERAL INFORMATION:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
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TYPE: DNA
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AGAAAGTAAATAAATAATTTATTCAT 228189
                            ACAAAAAACCATAAGACATTGTCCAT 365
                                                                                              CGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAAAACAACAACAAAAA
                                                                                                                              CCTGTAATCCCACTTACTCGGGAGGCAAAGGTTGCAATGAGCCCAGATTGCACCACTGCA
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GENERAL INFURFACION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 598906

LENGTH: 984
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; ORGANISM: Homo sapien US-10-301-480-1212315
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US-10-301-480-598906
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US-10-301-480-1212315
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1212315, Application US/10301480 Publication No. US20060057564A1
                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1212315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 201; Conserv
                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
                                                                                                                      PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
                                         TYPE: DNA
                                                              LENGTH:
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Pred. No. 1.9e-36;
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US-09-967-768A-314/c
US-09-967-768A-314/c
; Sequence 314, Application US/09967768A
; Patent No. US20020150877A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7647
LENGTH: 4388
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-7647
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US-09-764-891-7647/c
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Best Local S
Matches 201
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Sir
hes 202;
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                                                                                                                                                                                                                                                                                                                                              TCGAGACCAGCCTGGCCAACATGGTGAAACTCCGTCTCTACTAAAAATACAAAAATTAGC
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                                                                                                                  CARAAAAAAAAAAAAAAAAAAA 1021
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Pred. No. 5.3e-36;
1; Mismatches 52;
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Pred. No. 1.9e-36;
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APPLICANT: Munger, William E.
TITLE OF INVENTION: Identifying Drugs for and Di.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR PPLICATION NUMBER: 09/873,319
PRIOR FILING DATE: 2001-06-05
                                                                  ; OTHER INFORMATION: Genbank Accession No. US-09-960-706-969
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CURRENT APPLICATION NUMBER: US/09/967,768A

CURRENT FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: US/60/236,109

PRIOR APPLICATION NUMBER: US/60/236,034

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 969
LENGTO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 969, Application US/09960706 Publication No. US20030134280A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 314
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APPLICANT: Augustus
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TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Sets
                                                                                                           ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                         TYPE: DNA
                                                                                                                                                                            LENGTH: 174424
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Score 152; DB 3; Pred. No. 3e-35;
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Pred. No. 3e-35;
0; Mismatches
                                                                                    US20030134280A1 US2112
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RESULT 37
US-10-843-641A-6459/c
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Publication No. US20050064454A1
                                                                                                                                                                            uery Match
                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 8447
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PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Signature Gene Sets
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 689290-189
                                                                                                                                                                                                                   10-843-641A-6459
                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                          TYPE: DNA
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                                                             48438 TCCTCAGGTGTCTGGTGATCCTTGGTTGTCTTCTCATATTTAAGAATGGGGCAGGCTGGG
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FILING DATE: 2001-09-18
APPLICATION NUMBER: US/09/954,456
FILING DATE: 2001-09-25
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FILING DATE: 2001-10-02
APPLICATION NUMBER: US/09/969,347
FILING DATE: 2001-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/964,824
FILING DATE: 2001-09-27
APPLICATION NUMBER: US/09/967,768
FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/962,436
FILING DATE: 2001-09-25
APPLICATION NUMBER: US/09/962,832
FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/969,708
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-10-03
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66 CATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCA
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                                                                                               TACTCAGCCATGTGCTGGGCCATGGGAACCCCAAATATTAATAAGACATTGTCAGGCCAGG
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                                                                                                                                      Score 152; DB 1
Pred. No. 3e-35;
0; Mismatches
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US-10-723-860-2392/c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01 CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003.11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy
APPLICANT: Zlotnik, Albert
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PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
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                                      GAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                                               AATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCG 245
                                                                                                                                                                       CCTGAGGTCAAGACAAGTCCATCCTGGCCAACATGGTGAAACCCCTGTTTGTACTAAA 48264
                                                                                                                                                                                                                   CCTGAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAA 185
                                                                                                                                                                                                                                                                                                    CATGACACTGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCA 125
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ĠĀĠĠĊĀĠĠĀĠĀĀTĊĠĊŦŦĠĀĀTĊĊĠĠĠĀĠĠŦĠĠĀĠŦŦĠĊĀĠŦĠĀĠĊĊĠĀĠĀŦŦĠŦĠĊ 48146
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US-10-756-149-2215/c
US-10-756-149-2215/c
; Sequence 2215, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; ARPLICANT: Aziz, Natusha
; ARPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file

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US-09-925-065A-45529
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PLILING DATE: 2000-10-24
PRIOR PLILING DATE: 2000-11-20
PRIOR PLILING DATE: 2000-11-20
PRIOR PLILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
                                                                                                                                    Query Match 37.5
Best Local Similarity 74.2
Matches 224; Conservative
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APPLICANT: Wand, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: Patentin version 3.2
SEQ ID NO 2215
LENGTH: 181343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45529, Application US/09925065A
Publication No. US20040181048A1
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ORGANISM: Homo sapiens
-09-925-065A-45529
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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ORGANISM: Homo Sapiens
-10-756-149-2215
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                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                ENGTH: 599
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hes 214;
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143 GAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAATAGCTG
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                                           GCCTGTAATCCCAGCACTTTGGGAGGCTAAGGTGGGCGGATCACCTGAGGTCAGGAGTTC
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ilarity 71.8%;
Conservative
                                                                                                                                 Score 151.6; DB 4;
Pred. No. 4.2e-36;
2; Mismatches 56;
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Pred. No. 3.1e-35;
0; Mismatches 80
                                                                                                                                    56; Indels
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-36
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45529
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Best Local Similarity 74.2%;
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 599
TYPE: DNA
ORGANISM: Homo mapiens
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                                                                                                                                                                                                                                                                                GCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATC
                                                                                                                                          GGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCC----GGAGATTGCAGTGA
                                                                          GCTGAGATCGCAGAGTGAGCCGAAATCACAGATCA-----
                                                                                                                                                                                         GAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAATTAGCCG
                                              ACCCRGGAGGCAGAGGTTGCAGTGAGCCAAGATCACGCCACTGCACTTCAGCCTGGGTGA
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                                                                                                                                                                                                                                                                                                                                2:
                                                                                                                                                                                                                                                                                                                              Score 151.6; DB 5;
Pred. No. 4.2e-36;
2; Mismatches 56;
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FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 146767
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US-10-301-480-146767
Sequence 146767, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping
TITLE OF INVENTION: in the Human Genome
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US-10-301-480-760176
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US-10-301-480-146767
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Best Local
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
(CURRENT APPLICATION NUMBER: US/10/301,480
(CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
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74.2%;
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Pred. No. 4.2e-36;
2; Mismatches 56
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; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-10-301-480-760176
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                                                                                                                          , OTHER INFORMATION: Genbank Accession No. AC005082 US-10-450-826-93
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Best Local Simi
Matches 224;
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LENGTH: 599
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APPLICANT: Axe
APPLICANT: COO
APPLICANT: Jai
APPLICANT: Eis
                                                     Query Match
Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Publication No. US20040101818A1
                                                                                                                                                                                                                          SEQ ID NO 93
                                                                                                                                                                                                                                                                                                  APPLICANT: Mertz, Lawrence
TITLE OF INVENTION: Gene Expression Profiles Associated with
FILE REFERENCE: 044921-5039-WO
CURRENT APPLICATION NUMBER: US/10/450,826
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 60/255,882
PRIOR FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/285,691
PRIOR FILING DATE: 2001-04-24
NUMBER OF SEQ ID NOS: 149
                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                           FEATURE:
                                                                                                                                                                                                        LENGTH: 169739
125892 GGTAAGAAAATCTTAGTTAAAGATCTAAAGTTTGGCCAGGCACAGTGGCTAACGCCTGTA 125833
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                   GGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCCTGTA 89
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Eistein, Richard
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70.9%;
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                                                             Score 151.4; DB b;
Pred. No. 4.6e-35;
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Pred. No. 4.2e-36;
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                                                                                            Length 169739;
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SEQ ID NO 70
LENGTH: 133300
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(133300)
OTHER INFORMATION: n = A,T,C or
US-10-331-053-70
RESULT 46
US-10-995-561-13489/c
; Sequence 13489, App
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US-10-331-053-70 .
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Best Local Similarity
Matches 211; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and
FILE REFERENCE: 529452001100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/331,053
CURRENT FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 86
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                                                                                                                                                                                       CCGAGATCGCGTCACTGCACTCCAGCCTGGGCGA-----
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  Application US/10995561
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77.3%;
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Pred. No. 5.6e-35;
1; Mismatches 51
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RESULT 47
US-09-764-860-797/c
| Sequence 797, Application US/09764860
| Patent No. US20020094953A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins,
| FILE REFERENCE: PC008
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; ORGANISM: Homo sapiens
US-09-764-860-797
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Best Local Similarity
Matches 199; Conserv
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LENGTH: 195998
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF
                                                                                                        Query Match
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                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 1198
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004.11-24
NUMBER OF SEQ ID NOS: 85702
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NAME/KEY: misc_feature
LOCATION: (1)...(195998)

OTHER INFORMATION: n = A,T,C or G,
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                                                                                    Local Similarity
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                    ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
ACGCCTGTAATGCTAGCACTTTGGGAGGCCAAGGCGGAGGATCACTTGAGGTCAGGAGT 2378
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76.8%;
                                                                                  37.7%;
                                                                Score 150.6; DB 3;
Pred. No. 4.2e-35;
1; Mismatches 95;
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Pred. No. 6.5e-35;
1; Mismatches 51;
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BESULT 48  BS_10_77/c  BSQUENCE 797, Application US/10074095  BSQUENCE 797, Application US/10074095  PADLICANT: ROSEN et al.  APPLICANT: ROSEN et al.  APPLICANT: ROSEN ET 2001-07-14  FILE OF INVESTION NUMBER: US/10/074,095  CURRENT PERRENCE: PC0096C1  CURRENT PERRENCE: PC0096C1  CURRENT PILING DATE: 2000-02-04  PRIOR FILING DATE: 2000-02-04  PRIOR PILING DATE: 2000-05-28  PRIOR PILING DATE: 2000-07-11  PRIOR PILING DATE: 2000-07-11  PRIOR PILING DATE: 2000-07-11  PRIOR PILING DATE: 2000-07-12  PRIOR PILING DATE: 2000-07-12  PRIOR PILING DATE: 2000-07-14  PRIOR PILING DATE: 2000-07-14  PRIOR PILING DATE: 2000-07-14  PRIOR PILING DATE: 2000-08-14  PRIOR PILING DATE: 2000-08-1	141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAATAGC 200
FILING DATE: APPLICATION N	PRIOR APPLICATION NUMBER: 60/224,518 PRIOR FILING DATE: 2000-08-14 PRIOR APPLICATION NUMBER: 60/236,369 PRIOR APPLICATION NUMBER: 60/224,519 PRIOR APPLICATION NUMBER: 60/224,519 PRIOR FILLING DATE: 2000-08-14 PRIOR APPLICATION NUMBER: 60/220,964 PRIOR FILLING DATE: 2000-07-26 PRIOR FILLING DATE: 2000-10-20 PRIOR FILLING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/241,809 PRIOR FILLING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/236,327 PRIOR FILLING DATE: 2000-10-29 PRIOR FILLING DATE: 2000-10-29 PRIOR APPLICATION NUMBER: 60/241,785 PRIOR APPLICATION NUMBER: 60/244,617 PRIOR PILLING DATE: 2000-08-14

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R APPLICATION NUMBER: 60/232,080
PR FILING DATE: 2000-09-08
PR APPLICATION NUMBER: 60/231,414
PR APPLICATION NUMBER: 60/231,414
PR APPLICATION NUMBER: 60/231,244
PR FILING DATE: 2000-09-08
PR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR APPLICATION NUMBER: 60/249,217

BR FILLING DATE: 2000-11-17

DR APPLICATION NUMBER: 60/249,211

DR FILLING DATE: 2000-11-17

DR APPLICATION NUMBER: 60/249,215

DR FILLING DATE: 2000-11-17
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JR APPLICATION NOT THE DATE:
APPLICATION NUMBER: 60/241,826
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/241,786
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/241,221
                                                                                              FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,401
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/241,808
FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/231,242
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/232,081
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/232,400
                                                                                                                                                                                           FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,399
                                                                                                                                                                                                                                 FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/232,397
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,214
FILING DATE: 2000-11-17
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,244
FILING DATE: 2000-11-17
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,208
FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/215,135
FILING DATE: 2000-06-30
APPLICATION NUMBER: 60/225,266
                                                                                                                                                                                                                                                                                              FILING DATE: 2000-09-14
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FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/230,438
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SOPTWARE: PATENTIN Ver. 2
SEQ ID NO 797
LENGTH: 32146
TYPE: DNA
ORGANISM: Homo sapiens
US-10-212-872-797
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Best Local
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                             Matches
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC008C2
CURRENT APPLICATION NUMBER: US/10/212,872
CURRENT FILING DATE: 2002-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application removed - See File Wrapper NUMBER OF SEQ ID NOS: 1198
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PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                             Local Similarity
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CTTGAACCCGGGAGGCGGAGGTTGCAATGAGCCGAGATTGTACTACTGCAATGCAGAGAC
                                                                                     TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAG-------CCGGAGATTGC
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                                                                   AGGGCATGGTGGCGGCACCTGTAGTCCCAGCTGCTTGGGAGACTGAGCCAGGAGAATTG 225
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Pred. No. 4.2e-35;
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Pred. No. 4.2e-35;
1; Mismatches 95;
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APPLICANT: EISENBACH-SCHWARTZ, Michal
APPLICANT: COHEN, Irun R.
APPLICANT: BESERMAN, Pierre
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
APPLICANT: MOSONEGO, Alon
CURRENT MOSONEGO, Alon
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT APPLICATION NUMBER: US/09/893,348
CURRENT APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/314,161
PRIOR APPLICATION NUMBER: US 09/218,277
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOMBER: IL 124500
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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Search completed: July 17, Job time : 1466 secs
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US-09-893-348-9/c
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Best Local Similarity 72.1%;
Matches 196; Conservative
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ORGANISM: Homo sapiens
-09-893-348-9
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                                                                                       13288 AAAAAACTTCATCTCAAAAAAAAAGAAAGAAA 13257
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                                                                                                                    CAAAAACAACAACAAAAAAAAAAAAAACCATA 352
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                    2006, 22:44:38
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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RESULT 1
US-11-266-748A-23004
; Sequence 23004, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION UNMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR PILING DATE: 2004-11-03

PRIOR PRIOR DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03
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US-11-266-748A-204137/c
; Sequence 204137, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-23004
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SOFTWARE: PatentIn version 3
SEQ ID NO 23004
LENGTH: 216387
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OR APPLICATION NUMBER: ED 04105484.2
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: US 60/662,276
OR FILING DATE: 2005-03-14
OR APPLICATION NUMBER: US 60/700,293
OR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195718 CTTGAACCTGAGAGGCAGAGGGTGCAGTGAACCAAGATACTCCAGCCTAGTGACACAGCG 195777
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105483.4
FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105507.0
FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 04105485.
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Mulligan, Karl
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77.0%;
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Pred. No. 9.5e-24;
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Gaps

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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 204137
LENGTH: 1000
                                                                                                                                                                         PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 391815, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Homo Sapiens
:-11-266-748A-391815
                                                                                                    SEQ ID NO 391815
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (31918)
CURRENT PEPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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ORGANISM: Homo Sapiens
-11-266-748A-204137
                                                                                                                                 SOFTWARE: PatentIn version 3.3
                                                                                                                                               WILLING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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Local Similarity 74.4%;
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Pred. No. 7.2e-23;
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; Sequence 482533, Application US/11266748A
; Publication No. US20060134663A1
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version SEQ ID NO 482533
                                                                                                                                  Matches
                                                                                                                                                         Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2005-07-1
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harkin, Paul
APPLICANT: Johnston, P
APPLICANT: Mulligan, K
                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                           LENGTH: 1000
                                                                                                                                                       local Similarity
          141
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TCGAGACCATCCTGGCCAACATGGTGAAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGC
                                                                         ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                    ACGCCTGTAATCCCAGCACTTTGGGAGGTCAACGTGGGCAGATCACTTGAGTTCAGGAGT
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Mulligan, Karl
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                                                                                                                                                 37.4%;
74.0%;
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Pred. No. 1.6
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Pred. No. 1.6e-22;
1; Mismatches 62;
                                                                                                                                    Mismatches
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US-11-266-748A-118317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; Homo Sapiens; ORGANISM: Homo Sapiens
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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APPLICANT: Johnston, Patr
APPLICANT: Mulligan, Karl
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SOFTWARE: PatentIn version 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1000
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FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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                                                              CAGGCACCTGTAATCCCAGGTACTAGGGAGGCTTTTGAACCCAGGAGGCAGAGGTTGCAG
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: ED 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105483.4
PRIOR APPLICATION NUMBER: ED 04105483.9
PRIOR APPLICATION NUMBER: ED 04105483.9
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PRIOR APPLICATION NUMBER: ED 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: ED 04105484.2
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PRIOR APPLICATION NUMBER: ED 04105484.2
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US-11-266-748A-160481/c
US-11-266-748A-160481, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-160481
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LENGTH: 1000
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         AACAACAACAAAAAACAAAAAA 347
                                                    CGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGATTCAGTCTCAAA
                                                                                               ATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA
                                                                                                                                           CAGGCACCTGTAATCCCAGGTACTAGGGAGGCTTTTGAACCCAGGAGGCAGAGGTTGCAG
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Pred. No. 3.4e-22;
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RESULT 8
US-11-266-748A-474173/c

US-11-266-748A-474173, Application US/11266748A

| Publication No. US20060134663A1
| GENERAL INFORMATION:
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Matches
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LENGTH: 1000
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ORGANISM: Homo Sapiens
-11-266-748A-403127
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  APPLICANT: Harkin, Paul APPLICANT: Johnston, F
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                       AAAAAAAAAAAAAAAAAAAAA 999
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Johnston, Patrick
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Pred. No. 3.4e-22
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US-11-319-952-56

Sequence 56, Application US/11319952
Publication No. US20060134114A1
GENERAL INFORMATION:
APPLICANT: Yousef, George M.
APPLICANT: Diamandis, Eleftherios
TITLE OF INVENTION: Novel Human Kallikrein-Like

FILE REFERENCE: MTS3USA
CURRENT APPLICATION NUMBER: US/11/319,952
CURRENT FILING DATE: 2005-12-28

CURRENT FILING DATE: 2005-12-28
PRIOR APPLICATION NUMBER: US/09/936,271
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/CA00/00258

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Matches 221;
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LENGTH: 1000
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TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
CURRENT FILING DATE: 7005-11-03
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
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ORGANISM: Homo Sapiens
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APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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AAAAAAAAAAAAAAAAAAAAA 2
                        AACAACAACAAAAAACAAAAAAA 347
                                                                            CGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGATAGAGTGAGATTCAGTCTCAAA
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Pred. No. 3.4e-22;
l; Mismatches 93
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RESULT 10
US-11-266-748A-219455
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; ORGANISM: Homo sapiens
US-11-319-952-56
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Best Local Similarity
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publication No. US20060134663A1
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                SEQ ID NO 2
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
                                                         NUMBER OF SEQ ID NOS: 483996
                                                                      PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                             APPLICATION NUMBER: EP 04105485.9 FILING DATE: 2004-11-03
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219455
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                                   PatentIn version 3.3
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75.48;
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Pred. No. 4.2e-22;
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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Best Local
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                                                                         Matches
                                                                                                          Query Match
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PRIOR
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APPLICANT: Johnst
APPLICANT: Mullig
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
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ORGANISM: Homo Sapiens
                                                                                                                                                                  TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                         LENGTH:
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/700,293
                                                                                                                                                                                                                                                                                                                          FILING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2004-11-03
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                           ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
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Mulligan, Karl
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ACGCCTGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCAGGAGT
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75.4%;
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Pred. No. 4.4e-22;
                                                                         Score 147.2; | Pred. No. 4.4e
                                                                                            4.4e-22;
                                                                                                              DB 8;
                                                                           59;
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Sequence 1113, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
ROCETMANDED DATE: 2002-03-28
ROCETMANDED DATE: 2002-03-28
                                                                                                                              RESULT 13
US-11-266-748A-23290/c
Sequence 23290, Application US/11266748A
Publication No. US20060134663A1
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US-11-293-697-1113/c
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SEQ ID NO 1113
LENGTH: 2909
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                    GENERAL INFORMATION:
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
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Pred. No. 5.2e-22;
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US-11-266-748A-30503/c
US-11-266-748A-30503, Application US/11266748A
; Publication No. US20060134663A1
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US-11-266-748A-23290
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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SEQ ID NO 23290
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                                                                                                                                                                                                                                                                                   APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILLING DATE: 2005-11-03
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CURRENT APPLICATION NUMBER: US//1/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
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Local Similarity 78.5%;
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Pred. No. 9.1e-22;
D; Mismatches 48;
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FILING DATE:

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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-24156
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                                                           SEQ ID NO 24156
LENGTH: 3324
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PRIOR PILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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                                                                                                        SOFTWARE: PatentIn
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                        FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
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APPLICATION NUMBER: US 60/662,276
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72.7%;
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Pred. No. 1.1e-21;
1; Mismatches 70;
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Best Local Similarity
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Best Local Similarity
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2005-07-1
NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18
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ORGANISM: Homo
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TGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGG
                                                                                          CCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCC
                                                                                                                                       ACACAATTTTACATTAAGAAATACTGTGCAGGCCATGCGTGGTGGCTCAGGCCTGTAATC
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                                                                CCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCGGAGGTCAGGAGTTCGAGACCAGCC
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Pred. No. 1.4e
l; Mismatches
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Pred. No. 1.4e-21;
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US-11-266-748A-480818/c
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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SOFTWARE: PatentIn version 3.3
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TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 04105507.0 FILING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105485.9 FILING DATE: 2004-11-03
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FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                CCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAGACCATCC 152
                                                                   CACACACCTGTAGTCCCAGCTACTCAGGAG------CCGGAGATTGCAGTGAGCTGAG
                                                                                                                              TTGCCAACATAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGG
                                                                                                                                                                     TGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGCTGGGCATGGTGG
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ATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAAA 324
                                       CAGGCACCTGTAATCCCAGCTACTAGGGAGGCTTTTGAACCCAGGAGGCAGAGGTTGCAG
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Pred. No. 1.4e-21;
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GENERAL INFORMATION: APPLICANT: Harkin,

Johnston, Patrick

Pau.

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US-11-266-748A-206136/c
; Sequence 206136, Application US/11266748A
; Publication No. US20060134663A1
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; ORGANISM: Homo Sapiens
US-11-266-748A-60135
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US-11-266-748A-60135
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELLICATION NUMBER: EP 04105482.6
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105484.9
PRIOR PILLING DATE: 2004-11-03
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Matches 178;
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APPLICANT: Johnston, Patr
APPLICANT: Mulligan, Karl
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                     TTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                                                                                                                                                                      CAMAAATTAGCTGGGCGTGGTGGTGCACCTGTAGTCCCAGTTACTTAGGAGGCTGAGG
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76.1%;
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Pred. No. 2.2e-21;
0; Mismatches 56
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITITLE OF INVENTION: Transcriptome Microarray Technology and
ITITLE OF INVENTION: Methods of Using the Same
ITITLE OF INVENTION: Wethods of Using the Same
ITITLE OF INVENTION: US/11/266,748A
ICURRENT FILLING DATE: 2005-11-03
IPRIOR APPLICATION NUMBER: EP 04105479.2
IPRIOR APPLICATION NUMBER: EP 04105482.6
IPRIOR APPLICATION NUMBER: EP 04105482.6
IPRIOR APPLICATION NUMBER: EP 04105482.6
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TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
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                                                                                                                                                                                                                                               APPLICANT: Harkin, Paul
APPLICANT: Johnston, P
APPLICANT: Mulligan, K
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NUMBER OF SEQ ID NOS: 483996
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ORGANISM: Homo Sapiens
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OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105485.9
OR APPLICATION NUMBER: EP 04105484.2
OR APPLICATION NUMBER: EP 04105484.2
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: US 60/662,276
OR APPLICATION NUMBER: US 60/662,276
OR FILING DATE: 2005-03-14
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APPLICATION NUMBER: EP 04105483.4
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70.0%;
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0; Mismatches
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US-11-266-748A-198112/c
; Sequence 198112, Application US/11266748A
; Publication No. US20060134663A1
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PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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APPLICANT: Johnsto
APPLICANT: Mulliga
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APPLICATION NUMBER: US 60/662,276
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                                                                                       APPLICATION NUMBER: EP 04105485.9 FILING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105484.2
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                                 APPLICATION NUMBER: US 60/662,276 FILING DATE: 2005-03-14
                                                                       FILING DATE: 2004-11-03
                   APPLICATION NUMBER: US
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Mulligan, Karl
DATE:
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73.6%;
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Pred. No. 2.5e-
1; Mismatches
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RESULT 22
U9-11-266-748A-59101/c
                                                                                 Query Match
Tocal Similarity
Conserv
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                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-59101
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Best Local Similarity
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 198112
LENGTH: 1000
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102; (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version
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LENGTH: 96217
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ORGANISM: Homo Sapiens
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APPLICATION NUMBER: EP 04105485.9
FILING DATE: 2004-11-03
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ilarity 88.6%;
Conservative
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                                                                            Score 143; DB 8;
Pred. No. 4.2e-21;
0; Mismatches 20
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Pred. No. 3.3e-21;
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR APPLICATION NUMBER: EP 04105403.7
PRIOR APPLICATION NUMBER: EP 04105403.7
PRIOR APPLICATION NUMBER: EP 04105403.7
PRIOR APPLICATION NUMBER: EP 04105405.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105405.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105405.0
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELLCATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR PELLCATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILLING DATE: 2005-07-18
PRIOR FILLING DATE: 2005-07-18
PRIOR FILLING DATE: 2005-07-18
PRIOR FILLING DATE: 2005-07-18
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Best Local Similarity
Matches 209; Conserv
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APPLICANT: Johnston, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo Sapiens
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A 357
                                             GCTGAGGCAGGAGAATGGCGTGAACCCGGGAGTCGAGATCGCGCCACTGCACTCCAGCCT 1875
                                                                                        CCGGAGATTGCAGTGAGCTGAGATC-----GCAGAGTGAGCCGAAATCACAGATCACAG 296
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Pred. No. 4.2e-21;
1; Mismatches 85
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RESULT 25
US-11-266-748A-28208
; Sequence 28208, Application US/11266748A
; Publication No. US20060134663A1
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
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NUMBER OF SEQ ID NOS: 483996
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 35.7%;
Local Similarity 69.4%;
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APPLICATION NUMBER: EP 04105485.9
FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
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Pred. No. 4.2e-
1; Mismatches
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PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 28208
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APPLICANT: Mohnston, Patrick
APPLICANT: Mohnston, Patrick
APPLICANT: Mohligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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LOCATION: (836909)..(836909)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc_feature
LOCATION: (414394)..(414394)
OTHER INFORMATION: n is a, c
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OTHER INFORMATION: n is a, c,
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                                         264 GATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCCGTCTCAA 323
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73.0%;
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Pred. No. 5.8e-21;
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RESULT 27

US-11-266-748A-292231/c

; Sequence 292231, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:
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U$-11-266-748A-223929/c
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Best Local
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Publication No. US20060134663A1
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ORGANISM: Homo Sapiens
-11-266-748A-223929
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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207; Conserv
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Mulligan, Karl
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Pred. No. 4.5e-21;
1; Mismatches 82;
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RESULT 28
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PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
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Best Local S
Matches 207
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                  CTCAAAAAAAAAAAAAAAAAGAAAAGAAAATTCCCTTACTGTGCCTACTTGCCCCCTC
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Pred. No. 4.5
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6

Sequence 293957, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:

Paul

APPLICANT: Harkin, APPLICANT: Johnston APPLICANT: Mullig

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RESULT 29
US-11-266-748A-343660
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Publication No. US20060134663A1
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ORGANISM: Homo Sapiens
-11-266-748A-293957
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PRIOR
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILLING DATE: 2005-11-03
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PRIOR
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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ENGTH: 1000
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                                                                                                                                                                              APPLICATION NUMBER: EP 04105482.6 FILING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105483.4
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FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
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FILLING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105507.0
FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105485.9
FILING DATE: 2004-11-03
                                     APPLICATION NUMBER: EP 04105485.9 FILLING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105484.2 FILLING DATE: 2004-11-03
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APPLICATION NUMBER: EP 04105507.0
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APPLICATION NUMBER: US 60/662,276 FILING DATE: 2005-03-14
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Pred. No. 4.5e-
1; Mismatches
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; ORGANISM: Homo Sapiens
US-11-266-748A-343660
                                                          ; UKGANISM: Homo Sapiens
US-11-266-748A-345386
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US-11-266-748A-345386/c
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 34360
LENGTH: 1000
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Publication No. US20060134663A1
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Query Match
Best Local Similarity
                                                                                                                                                       SOFTWARE: PatentIn SEQ ID NO 345386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715
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73.0%;
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Pred. No. 4.5e-21;
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Score 142.4; DB 8 Pred. No. 4.5e-21;

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RBSULT 31
US-11-266-748A-403868/c
US-11-266-748A-403868, Application US/11266748A
US20060134663A1
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PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105507.0
PRIOR PRIOR DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1000
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
                                                                  145 GACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAAATAGCTGGG
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205 CATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGCTGAG
                                                                                                                         466 CTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGTTGGATCACCTGAGGTCAGGAGTTCAA
                                                                                                                                                                                                                  207;
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                                          GACCAGCCTGGCCAACACGGTGAAACCCCCATCTCTGCTAAAAATTACAAAAATTAGCTGGG
                                                                                                                                                                 CTGTAATCCCAGCACTTCGGGAGGCCAAGGTCGGCGGATCACCTGAGGTCAAGAGATCGA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCA-----
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                  35.6%;
                                                                                                                                                                                                           Score 142.4;
Pred. No. 4.5e
1; Mismatches
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                                                                                                                                                                                                           4.5e-21;
ches 82;
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105403.7
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
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PRIOR FILLING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR FILLING DATE: 2004-11-03
PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
PRIOR FILLING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 406117, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul APPLICANT: Johnston, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version SEQ ID NO 406117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
373
                                             298
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GTGAGCAGAGTGAGACKCCGTCTCAAAAACAACAACAAAAAAACAAAAAAAACCATAAGACA 357
                                                                                     CTTGAACTGGGGAGGCAGAGGTTGCAGTGAGACAAGATCACGTCACTGTACTCCAGCCTG 372
                                                                                                                              AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCA-----CAGA
                                                                                                                                                                                                                         TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGA-----GCCGGAGATTGC 253
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                                                                                                                                                                                TGGGCATGATGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTG 312
                                                                                                                                                                                                                                                                        TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTATTAAAAATACAAAATTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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73.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Pred. No. 4.5e-21;
L; Mismatches 57;
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432
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RESULT 34

US-11-266-748A-477163/c

US-11-266-748A-477163/c

; Sequence 477163, Application US/11266748A
; Publication No. US20060134663A1
; DEPLICANT: Harkin, Paul
; APPLICANT: Harkin, Paul
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; ORGANISM: Homo Sapiens
US-11-266-748A-474914
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PRIOR PILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PRILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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Best Local Similarity

Matches 207; Conserv
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                             319
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Mulligan, Karl
                                                                                                                                                                                                                                                       CTCAAAAAAAAAAAAAAAGAAAAGTTCCCTTACTGTGCCTACTTGCCCCTC
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Pred. No. 4.5e
1; Mismatches
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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US-11-191-644-1
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                                                             APPLICANT: MICHAUD, GREG
APPLICANT: MICHAUD, GREG
TITLE OF INVENTION: COMPOSITIONS, KITS AND ITTLE OF INVENTION: DIRECTED TO CORTACTIN ITTLE OF INVENTION: DIRECTED TO CORTACTIN ITTLE REFERENCE: INV-1007-UT
CURRENT APPLICATION NUMBER: US/11/191,644
CURRENT FILLING DATE: 2005-07-27
PRIOR APPLICATION NUMBER: 60/591,827
PRIOR FILING DATE: 2004-07-27
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/11191644
Publication No. US20060141529A1
GENERAL INFORMATION:
APPLICANT: KOLESKE, ANTHONY JOHN
APPLICANT: BOYLE, SCOTT NILE
APPLICANT: HOYLE, SCOTT NILE
                   SOFTWARE: PatentIn version 3.3 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                              APPLICANT:
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2005-07-18
LENGTH: 157866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCA------CAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868 ATGCCTGTAATCCCAGCACTATGGGAGGCCAGGGAGGAGGATCTCCAGAGGTCAGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGA-----
                                                                                                                                                                                                                                                                                                    SCHWEITZER, BARRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTGAACTGGGGAGGCAGAGGTTGCAGTGAGACAAGATCACGTCACTGTACTCCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTATTAAAAATACAAAAATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGCATGATGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142.4; DB 8
Pred. No. 4.5e-21;
1; Mismatches 57
                                                                                                                                                                                                            CORTACTIN
                                                                                                                                                                                                              ASSAYS
AND AN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                              CONTAINING REAGENTS ARG/ABL PROTEIN KINASE
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무요문
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens -11-293-697-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -11-293-697-23/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -11-191-644-1
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62884 ACTGTCTTCTG 62894
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                                                                                                    196 ATAGCTGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCGGAGATTGCAG
                                                                                                                                                                                     136 AGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAA 195
                                                                                                                                                                                                                                       847 GTTTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTGAGGTCA
                                                                                                                                                            787 GGAGTTCGAGACCAGCCTGGCCAACATGGTGAAAACCCCGTCTCTACTAAAAAATACAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
667 AATCACTGGAACCCGGGAGGCGGAGGCCTC----CAGTCTAGTCAAAAAAAAAGCAAGACTC
                                                                                                                                                                                                                                                                                                                           198;
                                     256 TGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTCGGGGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTTTACTAAAAATACAAAAAATAGC
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                                                                               TTAGCTGGGCGTGGCACATGCCTGTAATCCCAGCTACCCGGGAGGCTGAGGCAGGAG
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73.6%;
                                                                                                                                                                                                                                                                                                                    Score 142; DB 8;
Pred. No. 5.7e-21;
1; Mismatches 71
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Pred. No. 6.3e-21;
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; ORGANISM: Homo
US-11-293-697-604
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US-11-293-697-604/c
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SEQ ID NO 604
LENGTH: 3252
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
                                                                                                                                                                                                                                                                                          Local Similarity
les 172; Conserv
                                                                                                                                            2878
2758 TGAGATCATGCCACTGCCCTCCAGCGTGGGCGACAGAGTGAG 2717
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                                TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAG 302
                                                                       CAGGCGTGGTGCTGCCTGTAATCCCCAGCTACTCGAGAGGCTGAGGTTGCAGTGAGC
                                                                                              TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCCGGAGATTGCCAGTGAGC
                                                                                                                                                                          TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAATAGC
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                                                                                                                                            TTGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAATAAAACAAAAATTAGC
                                                                                                                                                                                                                  ACGCCTGTAATCCCAGTACTTTGGGAGGCTGAGGGAGGTGGATCACGTGAGGTCAGGAGT
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o. US20060105376A1
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                                                                                                                                                                                                                                                                                        Score 142; DB 8;
Pred. No. 5.7e-21;
D; Mismatches 50
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                                                                                                                                                                                                                                                                                                                          Length 3252;
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RESULT 38
US-11-266-748A-202571
| Sequence 202571, Application US/11266748A
| Publication No. US20060134663A1
| APPLICANT: Horkin, Paul
| APPLICANT: Johnston, Patrick
| APPLICANT: Johnston, Patrick
| APPLICANT: Mulligan, Karl
| TITLE OF INVENTION: Methods of Using the Same
| FILE REFERENCE: 55815-0102 (319189)
| CURRENT APPLICATION NUMBER: US/11/266,748A
| CURRENT FILING DATE: -2005-11-03
| PRIOR APPLICATION NUMBER: EP 04105492.6
| PRIOR APPLICATION NUMBER: EP 04105403.4
| PRIOR FILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105403.4
| PRIOR FILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105405.9
| PRIOR APPLICATION NUMBER: EP 04105404.2
| PRIOR APPLICATION NUMBER: EP 04105404.2
| PRIOR APPLICATION NUMBER: EP 04105404.2
| PRIOR FILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105404.2
| PRIOR FILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105404.2
| PRIOR FILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105404.2
| PRIOR FILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105404.2
| PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3

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RESULT 39
US-11-266-748A-23004/c
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LENGTH: 1000
  Query Match
                                           -11-266-748A-23004
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                 PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENERAL INFORMATION
                                                                                                                                                  SOFTWARE: Patentin
                                                                                                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR TILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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ORGANISM: Homo Sapiens
                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                      ENGTH: 216387
                                                                                                                            ID NO 23004
                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 04105485.9
FILLING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
FILLING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTCAAAAACAACAACAAAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAACTTGGGAGGTGAAGGTTGCAGTAAGCCACTCCAGCCTGGGTGACAGAGTGAGACTTT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAG-----CCGGAGATTGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGACCATCCTGGCCAACATGGCGAAACCCCCGTCTCTACCAAAAATAGAAAAATTAGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCTGGAATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAGAGTGAGACKCC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATGGTGGCACATGTTTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTT 562
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  35.4%;
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Pred. No. 6.5e-21;
1; Mismatches 60;
    Score 141.6;
    B
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Length 216387;
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CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR TILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                 SEQ ID NO 201568
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                                                                                                                                                      Matches 172;
                                                                                                                                                                         Query Match
Best Local
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR TITLY DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2005-03-14 PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                           LENGTH: 632
                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87783
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/662,276
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                                 86
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                               TGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGATCGAG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGCAGGAGAATCACCTGAACCTGGGTGGTGGAGGCTGCAGTGAGCAGAGATCGTGCCA 87664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGATTGCAGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGCAG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATATAAAAATTAGTCGGGCATGGTGGCACATGCCTGTAATCCCAGCTACTCATGAGGCT 87724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAA
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                                                                        CATGGGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACACTGGCTGAATGCC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATACAAAAAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCAGCTACTCAGGAGCCG 245
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77.1%;
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1; Mismatches 85;
                                                                                                                                                                         Score 141.4; DB Pred. No. 7e-21;
                                                                                                                                                      Mismatches
                                                                                                                                                                                            DB 8;
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ACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAAAATAGCTGGGC 205

APPLICANT:

MODEL,

Fabian

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RESULT 42
US-10-517-441-32/c
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
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Matches
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:
                                                                                                         GENERAL INFORMATION:
                                                                                                                           Sequence 32, Application US/10517441 Publication No. US20060121467A1
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ORGANISM: Homo Sapiens
-11-266-748A-59943
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SOFTWARE: PatentIn version 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                     201 TGGGCATGGTGGCACACCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154;
                    : FOEKENS, John
: HARBECK, Nadia
: KOENIG, Thomas
: MAIER, Sabine
                                                                                                                                                                                                                                                        CAGGCATGGTGGCGGACACCTGTAATCCCAGCTACCCAGGAGGCTGAGGCAGGAG
                                                                                                                                                                                                                                                                                                                                           TCGAGACCAGCCTGGCCAATATGGTGAAACCCCCGTCTTTACTAAAAATACAAAAATTACC
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Mulligan, Karl
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Pred. No. 7.5e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8;
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APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

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US-11-266-748A-60244
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR APPLICATION NUMBER: DE 10345779.4
PRIOR FILING DATE: 2003-01-07
PRIOR PILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60244, Application US/11266748A Publication No. US20060134663A1
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PRIOR APPLICATION NUMBER: EP 04105485.9 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105484.2 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: US 60/662,276 PRIOR FILING DATE: 2005-03-14
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APPLICANT: Johnsto
APPLICANT: Mullig
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APPLICANT:
APPLICANT:
                                                                                                                                           PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR FILING DATE: 2004-11-03
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TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 154; Conserv
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RUJAN, Tamas
SCHMITT, Armin
SCHMITT, Manfred
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Pred. No. 7.9e-21;
0; Mismatches 21;
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US 60/700,293

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US-11-266-748A-23291/c
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Query Match
Best Local Similarity
                                                               -11-266-748A-23291
                                                                                                                                             SEQ ID NO 23291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnston, Patrick APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-60244
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NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                              LENGTH: 113853
TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                   OR APPLICATION NUMBER: EP 04105482.6
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105483.4
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105507.0
OR FILING DATE: 2004-11-03
OR APPLICATION NUMBER: EP 04105485.9
OR APPLICATION NUMBER: EP 04105485.9
OR FILING DATE: 2004-11-03
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les 206; Conserv
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                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
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72.3%;
    35.4%;
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    Score 141.4; DB 8; Pred. No. 9.1e-21;
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                        Length 113853;
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-58517
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 172; Conserv
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR FILING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105485.9 PRIOR FILING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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139180 CTTGAACATGGAAGGTGCAGGTTGCAGTGAGCTGAGATTGTGC 139138
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                                                                                                                                                                         139300
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                                                                                                              TGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGCAGTGAGC
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                                        TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                                                                                                       TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAACACACAAAAATAAGC
                                                                                   TGGGCGTGGTGGCGCACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCA 139181
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                                                                                                                                                                                                                                                                                                                                          Score 141.4; Db o;
Pred. No. 9.2e-21;
""smatches 51;
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Milligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 47
                                                                                                                                                                                                                                                                                Sequence 24937, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 22662
                                   APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
-11-266-748A-22662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                       -11-266-748A-24937/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 164429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27432 CTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATCGTGC 27390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 04105507.0 FILING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105485.9 FILING DATE: 2004-11-03 APPLICATION NUMBER: EP 04105484.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 ATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGTCAAGAGA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAAATACAAAAAAATAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCAGGAGT 27553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGCATGGTGGCACACCCTGTAGTCCCAGCTACTCAGGAGCCCGGAGATTGCAGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGAGACCAGCCTGGCCAACATGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGC
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77.1%;
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Pred. No. 9.3e-21;
0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 164429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3 SEQ ID NO 24937
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.3%;
Best Local Similarity 67.9%;
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                             67263
67143 ACAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGATTGTGC
                                                                                                                                                                                                                                                                       67323 GGTGATCATGCCTGTAATCCCAGCACTTTAGGAGGCTGAGGCGGGTGGATCACCTGAGGT
                                                                                                                                                                                                                                                                                                                                                              67383 CATTTATTGTTTCTTTTAAATGAACAAAATTTAGAGAAAAGTTATTCCAGGCCAGGCAT 67324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105483.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 04105482.6
                                                                                                                   194 AAATAGCTGGGCATGGTGGCACACACCTGTAGTCCCCAGCTACTCAGGAGCCGGAGATTGC
                                                                                                                                                                                                          134 CAAGAGATCGAGACCATCCTGGCCAACATGGTGAAACCCCCGTCTTTACTAAAAATACAAA 193
                                          254
                                                                                                                                                                                                                                                                                                                 74 TGGCTGAATGCCTGTAATCCCAGCACTTCGGGAGGCCAAGGTGGGCGGATCACCTGAGGT 133
                                                                                                                                                                                                                                                                                                                                                                                                        14 CATGTGCTGGGCCATGGGAACCCAAATATTAATAAGACATTGTCAGGCCAGGCATGACAC
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                                                                                                                                                                           CAGGAGTTCGAGACCAGCCTAGCCAACATGGTGCAACCCTGTCTCTACTAAAAATACAAA
                                       AGTGAGCTGAGATCGCAGAGTGAGCCGAAATCACAGATCACAGAGTGAGC 303
                                                                                         AATTAGCCGGGCATGGTGATGTAAGTCTGTAGTCCCAGCTACTCAGGAGGCTGAGGTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141.2; DB Pred. No. 9.9e-21); Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 86215;
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67094
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RESULT 48

US-11-266-748A-119261

Sequence 119261, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

ITILE OF INVENTION: Methods of Using the Same

ITILE OF INVENTION: Methods of Using the Same

PILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR APPLICATION NUMBER: EP 04105484.2

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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Techr
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT PILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 04062,276
PRIOR APPLICATION NUMBER: US 00/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
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US-11-266-748A-161425/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 161425, Application US/11266748A publication No. US20060134663A1 GENERAL INFORMATION:
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SEQ ID NO 119261
LENGTH: 1000
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 161425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo Sapiens
·11-266-748A-119261
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Harkin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCGGAGGTAGAGGTTGCAGTGAGCCGAGATCGCAACACTACACTCCAGCCTGGGCGAC
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Pred. No. 8.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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US-11-266-748A-407602

ORGANISM: Homo Sapiens

LENGTH: 10

1000

SOFTWARE: PatentIn version SEQ ID NO 407602

PRIOR FILING DATE: 2005-07-18 NUMBER OF SEQ ID NOS: 483996

Query Match
Best Local Similarity
Matches 229; Conser

35.3%; ilarity 68.8%; Conservative

Score 141; DB 8; Length 1000; Pred. No. 8.7e-21; 1; Mismatches 86; Indels 1

17;

Gaps

2

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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PRIOR DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sa
US-11-266-748A-161425
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US-11-266-748A-407602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 407602, Application US/11266748A Publication No. US20060134663A1
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Best Local
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APPLICANT: Johnston, P
APPLICANT: Mulligan, K
                                                                                                          PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR FILING DATE: 2004-11-03 PRIOR PELICATION NUMBER: EP 04105485.9 PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
                                      PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
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